

Mon Sep 9 09:30:05 2002

us-09-834-291-1.rge

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
 Run on: September 7, 2002, 10:21:41 ; Search time 12179.2 Seconds
 (without alignments)
 5518.916 Million cell updates/sec

US-09-834-291-1
1 tgcagactctcagataatg.....ttgcagatgctcaatcaag 3212

Title: 3212
 Sequence: 1 tgcagactctcagataatg.....ttgcagatgctcaatcaag 3212

Scoring table: IDENTITY_NDC
 Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
 Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database: GenEmbl:
 1: gb_ba:*
 2: gb_hlg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
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 11: gb_sts:*
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 13: gb_un:*
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 16: em_fun:*
 17: em_hum:*
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 27: em_sts:*
 28: em_un:*
 29: em_vl:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htgo_inv:*

Pred. NO. is the number of results predicted by chance to have a
 score greater than or equal to the total score distribution.
 and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
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Result No.	Score	Query Match	Length	DB ID	Description
1	3212	100.0	3212	6	AX026089
2	3185	99.2	187313	6	AL157394
3	2346.6	73.1	2827	6	AX026092
4	2211.8	68.9	2344	9	HSCD955FR
5	2133.4	66.7	2165	9	HUMFAS
6	1899.6	59.1	1877	6	AX026091
7	1850.8	57.6	1380	9	HSPASX1
8	1536.8	47.8	1608	6	AX347321
9	961	29.9	1608	6	AX347320
10	957.4	29.8	1608	6	AX347320
11	713	22.6	720	6	AX026090
12	698.8	21.6	702	9	HSAT29012
13	697.2	21.7	702	9	HSAT29013
14	695.6	21.7	702	9	HSAT29013
15	342	10.6	2719	9	BC012479
16	262.8	8.2	266	6	AX026120
17	262.8	8.2	266	6	HSK011034
18	257	8.0	398	11	G27038
19	252	7.8	251	6	ARI43111
20	252	7.8	251	6	HSAP01
21	226	7.0	2471	6	I58632
22	226	7.0	2471	6	I58632
23	226	7.0	2534	6	A87646
24	226	7.0	2534	6	ARI63572
25	226	7.0	2534	6	ARI73438
26	226	7.0	2534	6	ARI73438
27	226	7.0	2534	6	ARI73438
28	226	7.0	2534	6	ARI73438
29	208.6	6.5	7218	4	HUMFASANT
30	79.4	2.5	16494	4	EU0121
31	78.6	2.4	16494	4	EU0121
32	73.8	2.3	17387	2	AF267170
33	73.8	2.3	17387	2	AF267170
34	73.8	2.3	17387	2	AF267170
35	73.8	2.3	17387	2	AF267170
36	73.8	2.3	17387	2	AF267170
37	73.8	2.3	17387	2	AF267170
38	70.6	2.2	125020	9	AC008542
39	70.6	2.2	125020	9	AC008542
40	69.8	2.2	125020	9	AC008542
41	69.8	2.2	125020	9	AC008542
42	69.8	2.2	125020	9	AC008542
43	69.8	2.2	125020	9	AC008542
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45	69.8	2.2	125020	9	AC008542

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	3212	100.0	3212	6	AX026089
2	3185	99.2	187313	6	AL157394
3	2346.6	73.1	2827	6	AX026092
4	2211.8	68.9	2344	9	HSCD955FR
5	2133.4	66.7	2165	9	HUMFAS
6	1899.6	59.1	1877	6	AX026091
7	1850.8	57.6	1380	9	HSPASX1
8	1536.8	47.8	1608	6	AX347321
9	961	29.9	1608	6	AX347320
10	957.4	29.8	1608	6	AX347320
11	713	22.6	720	6	AX026090
12	698.8	21.6	702	9	HSAT29012
13	697.2	21.7	702	9	HSAT29013
14	695.6	21.7	702	9	HSAT29013
15	342	10.6	2719	9	BC012479
16	262.8	8.2	266	6	AX026120
17	262.8	8.2	266	6	HSK011034
18	257	8.0	398	11	G27038
19	252	7.8	251	6	ARI43111
20	252	7.8	251	6	HSAP01
21	226	7.0	2471	6	I58632
22	226	7.0	2471	6	I58632
23	226	7.0	2534	6	A87646
24	226	7.0	2534	6	ARI63572
25	226	7.0	2534	6	ARI73438
26	226	7.0	2534	6	ARI73438
27	226	7.0	2534	6	ARI73438
28	226	7.0	2534	6	ARI73438
29	208.6	6.5	7218	4	HUMFASANT
30	79.4	2.5	16494	4	EU0121
31	78.6	2.4	16494	4	EU0121
32	73.8	2.3	17387	2	AF267170
33	73.8	2.3	17387	2	AF267170
34	73.8	2.3	17387	2	AF267170
35	73.8	2.3	17387	2	AF267170
36	73.8	2.3	17387	2	AF267170
37	73.8	2.3	17387	2	AF267170
38	70.6	2.2	125020	9	AC008542
39	70.6	2.2	125020	9	AC008542
40	69.8	2.2	125020	9	AC008542
41	69.8	2.2	125020	9	AC008542
42	69.8	2.2	125020	9	AC008542
43	69.8	2.2	125020	9	AC008542
44	69.8	2.2	125020	9	AC008542
45	69.8	2.2	125020	9	AC008542

BASE COUNT

ORIGIN

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 3212; DB 6; Length 3212;
Matches 3212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 tgaagactctcaggaatctgctgtaaaataaataaactcttagagatgcccactgtc 60
QY 61 ttcccccaggaacacagcattcattggtgtcattcaatagattcttcaagatcca 120
DB 61 ttcccccaggaacacacagcattcattggtgtcattcaatagattcttcaagatcca 120
QY 121 aagcaagaagaagtttggggaacagatataaataccaccccttgacatagacac 180
DB 121 aagcaagaagaagtttggggaacagatataaataccaccccttgacatagacac 180
QY 181 taagggccctgagaagtttgattagaagaagtttcaaatgaagtaaccagaatttc 240
DB 181 taagggccctgagaagtttgattagaagaagtttcaaatgaagtaaccagaatttc 240
QY 241 ctaagattatctgacatgaacataatgctcccccagaagacataatctctacc 300
DB 241 ctaagattatctgacatgaacataatgctcccccagaagacataatctctacc 300
QY 301 gaacttgagaataatgaagcgtacgtggtagagggtaggggaaggggtatagacata 360
DB 301 gaacttgagaataatgaagcgtacgtggtagagggtaggggaaggggtatagacata 360
QY 361 aagcagagagacttgaggaagaagaataatgaagtttaactctgacatctatatta 420
DB 361 aagcagagagacttgaggaagaagaataatgaagtttaactctgacatctatatta 420
QY 421 actaacacactctgcaatgctgtaagctcttcttgacagctcttcttcttcttct 480
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QY 541 caactatgtagtctgctgctataatcaactcaagaagtaactgacttctgcaatt 600
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QY 601 ccttccctcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 660
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DB 661 ctccctcaac 720
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DB 721 attctggaatagtttaggaattcaaaaatttgcagagaataacagaagaatgccc 780
QY 781 taacatctctcttcttcttcttcttcttcttcttcttcttcttcttcttctt 840
DB 781 taacatctctcttcttcttcttcttcttcttcttcttcttcttcttcttctt 840
QY 841 ggtctgcaagcccaaggtcttctctatagcaactcaagcttaactgaagaatgaca 900
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QY 961 gtgatgaaagagcctcagagggtaacctaaactagattgaagcccaacagagctcag 1020
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DB 1021 aagaataatcactgaaggaagcctgaagatgaacagctggctaaagaggtat 1080
QY 1081 taatgttataatggttgaatccttaattgggaaggaagaggttgcagagtggtg 1140
DB 1081 taatgttataatggttgaatccttaattgggaaggaagaggttgcagagtggtg 1140
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DB 1141 cagaagcttgtagcagatgaagcaagaatactgaacacttgatgctcagctgagc 1200
QY 1201 tgcattccaaatcaggtcagatgaatgcaatccaaacatacctctgtaaatc 1260
DB 1201 tgcattccaaatcaggtcagatgaatgcaatccaaacatacctctgtaaatc 1260
QY 1261 atgctaaactcaactgaagctctacccgtccaaagcaatagcttgaagcttgc 1320
DB 1261 atgctaaactcaactgaagctctacccgtccaaagcaatagcttgaagcttgc 1320
QY 1321 cccagagacagaaagaattacaagaatttctttaaagaataatgagcagagaat 1380
DB 1321 cccagagacagaaagaattacaagaatttctttaaagaataatgagcagagaat 1380
QY 1381 agtaagagagagaggaagtaattgtaatttcaatagcttgggctatgagattg 1440
DB 1381 agtaagagagagaggaagtaattgtaatttcaatagcttgggctatgagattg 1440
QY 1441 cttaagttgctgcttcttcttcttcttcttcttcttcttcttcttcttctt 1500
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DB 1801 actgaggaagcagcagcaggaatgccaatctgtgcaagaacactgactctcc 1860
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Page 4

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Mon Sep 9 09:30:05 2002

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RESULT 4
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 VERSION beta interferon; CD95 gene; silencer.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2344)
 Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and Watson, J.
 Identification of a silencer, enhancer, and basal promoter region in the human CD95 (Fas/PO-1) gene
 JOURNAL D.N.A. Cell Biol. 14 (11), 931-937 (1995)
 MEDLINE 96069539
 REFERENCE 2 (bases 1 to 2344)
 Rudert, F.H.
 Direct Submission
 TITLE Submitted (26-May-1995) F.H. Rudert, Genesis Research & Development, Corporation Ltd., PO Box 150, Auckland, NEW ZEALAND
 JOURNAL Overlaps with X81335, & X82279-X82286
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 Db 178 TTTCCCGAAGACACACATCTCATTTAGGTGTTCTATCATATAGATCTTCAAGATTTCCA 237
 QY 121 aaggaagaagatttggggaacagatatataattacccacccttgaacattagcattac 180
 Db 238 AAGGCAAAATAATTGGGGAACAGATATATATATACCAACCTTTGACATTAAGCATA 297
 QY 181 taaggccctggagaagtttggattaaagaagtttcaatttaagaagaccagaattt 240
 Db 298 TAAGGGCCCTGAGAGATTTTGATTAAGAAAGTTTCAATTAAGATACCCAGAAATTTT 357
 QY 241 ctgaattatttgaacataaagaataatgctcccccacaaagacatatcttctccct 300
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 QY 301 gaacttgaagataatagacgtacgtgtagaggttaggggaaggggtatgacataga 477
 Db 418 GAAGGAGGATTAATTAAGAGCTAGCTAGTGAAGGTAGGGAAGGGGTATGCGATAGA 420
 QY 361 aagagcaagaccttgggggaagaagataataaatttaattcctgactcgtattatata 480
 Db 478 AAGAGCAGACCTTGGGAGCAAGAAATATCTAATTTCTGACTCTGCTATTTATTA 537
 QY 421 actaacacatcttgcacatgcttgaagcttcttggctacattttttatttgaagaa 597
 Db 538 ACTAACCATTGTCGCAAGTGTCTTAAGCTTTTGGCTCATTTTATTTATTTGTAAG 657
 QY 481 taagtttaataacactcactcactcactcactcactcactcactcactcactcactc 600
 Db 598 TAACTTAATTAATCACTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCAT 657
 QY 541 cacaatagtagtctgctgtcttataatcactcactcactcactcactcactcactc 717
 Db 658 CACATATGTGATGTGCTGCTATTAATTAATCACTCAAGAGATATCAATTTGCAATGT 777
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	ACCESSION	D31968		
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	TITLE	Nakanishi,Y.		
	AUTHORS	Direct Submission		
	JOURNAL	Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences, 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@db.s.p.kanazawa-u.ac.jp, Tel:076-334-4424, Fax:076-234-4480) Location/Qualifiers 1. .2165 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="pF7" /issue_type="Blood" 79. .87 protein_bind		
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Db 301	AAAAATTCACAGATATATACAGAAATGCCATATACCATCTCTCTATCCACTCTCTT	806		
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Db 361	TTGTGTCTATTATGATATCTCAGAGTGTGTGCACAAAGGTGTGGCAAGCCCAAGGTC	866		
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REFERENCE	1 (sites)		
AUTHORS	Olek, A., Piepenbrock, C. and Berlin, K.		
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 702)			
AUTHORS	Muschen, M., Re.D., Jungnickel, B., Diehl, V., Rajewsky, K. and Kuppers, R.			

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS
Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction	Unpublished	2 (bases 1 to 702)	Muschen, M., Re, D., Brauning, A., Wolf, J., Hansmann, M., Diehl, V., Kuppers, R. and Rajewsky, K.	Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg cells	Unpublished	3 (bases 1 to 702)	Muschen, M.
Direct Submission	Submitted (19-SEP-2000)	Submitted for Genetics, LFI E4 R705, Joseph-Steilzmann-Str. 9, 50931 Köln, GFRMANY		Related sequences: D31968 X89101 AJ279012 AJ279013			
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Mon Sep 9 09:30:05 2002

us-09-834-291-1.rge

Page 19

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VERSION BC012479.1 GI:15214691
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REFERENCE 1 (bases 1 to 2719)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
REMARK Contact: MGC help desk
COMMENT Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villaloboscm.tmc.edu
Villalon, D.K., Luna, R.A., Haley, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
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Best local Similarity 100.0%; Pred. No. 7; Le-69;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1917 agccctcccaacccgggggttcctcccaagcagagctctccctccatctctcgaacacgg 1976
|||||
DB 1 AGCCCTCCCAACCCGGGGTTCCTCCACGAGGAGCTCTCCATCTCTGACACCGG 60
QY 1977 ggcttcgtgaagctcgtctcgtatcgcgaagaagtacacacaggtgtcaagaagc 2036
|||||

DB 61 GGCCTTTCGTAGCTCGCTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTCAAGAGC 120
QY 2037 cttctgggagtgaggaagcaggttctagagtgactgtgagcctcgaaggcgagca 2096
|||||
DB 121 CTCTGGGAGGTGAGGAGGAGGCTTTACGAGTACTTGCTGGAGCCTCAGGGGCGGCA 180
QY 2097 ctggcagcgaacacacacccctgagccagccctgtgtgcccagggcgagctgctcttc 2156
DB 181 CTGGCAGGAAACACACCCCTGAGCCAGCCCTGGCTGCCAGCGGAGCTGCTCTCTCC 240
QY 2157 egcggttggtgagccgctcagtagcaggttgaggagctcttcaacttcgaagattg 2216
|||||
DB 241 CCGGGGTGTGTGACCCGCTCAGTACGAGATTGGGGAAGCTTTCACTTCGAGGATTG 300
QY 2217 ctcaacaacatgctggtgcatctggaacctctactctgt 2258
|||||
DB 301 CTCACCAACCATGCTGGGATCTGGACCTCCTACCTCTGAT 342

Search completed: September 7, 2002, 18:21:38
Job time: 28797 sec

1

Human nervous syst

```
/*tag= e
```


PN WO200200928-A2.

PD 03-JAN-2002.

PF 02-JUL-2001; 2001WO-EP07557.

PR 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Beiln K;

XX WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful

PT for diagnosis and treatment of diseases associated with abnormal

PT cytosine methylation

PS Claim 1; SEQ ID NO 2391, 32pp + Sequence Listing; German.

XX

XX

CC The present invention provides a number of human immune system associated

CC genes which are modified by the methylation of cytosines.

CC can be used in the diagnosis and treatment of immune system associated

CC including eye diseases such as retinopathy, neovascular glaucoma and

CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

CC rheumatoid arthritis, psoriasis and inflammatory/autoimmune diseases.

XX The present sequence is a gene of the invention.

XX Sequence 1608 BP; 398 A; 51 C; 423 G; 736 T; 0 other.

Query Match

Best Local Similarity 29.8%; Score 957.4; DB 24; Length 1608;

Matches 1215; Conservative 0; Mismatches 371; Indels 5; Gaps 3;

QY 779 tataacatccctccctaccacactctctttgtgctcattagatgctcagagtggtgac 838

DB 19 tatatatctctccctaccacactctctttgtgctcattagatgctcagagtggtgac 838

QY 839 aaggtgacacagccagagctcctcccatagagcactaacagctcactgaagtggtgac 898

DB 79 aaggtgacacagccagagctcctcccatagagcactaacagctcactgaagtggtgac 898

QY 899 agaacagccatcaaacactcaaacagactggtgtaagtcagtgacagtgacagtgacag 138

DB 139 agtaagttacttaataattataagaatggtgtaagtcagtgacagtgacagtgacag 138

QY 959 ggtgatggaagccctcagaggggtaacctactgatttgagggtcccaagagctc 198

DB 199 ggtgatggaagccctcagaggggtaacctactgatttgagggtcccaagagctc 198

QY 1018 cagagaanaatgcgaactggaaggaagagcgaaggaatggaacgtggcctcaagcaaaaggt 1077

DB 259 tagaagaanaatgtaattgagaggaaggttgaaggaatgagtggtgtaagtaaaaggt 1077

QY 1078 tattaatgtctataatggttgcgaatcaatctgggaaggaaggaaggttgcgaatgag 1137

DB 319 tattaatgtctataatggttgcgaatcaatctgggaaggaaggaaggttgcgaatgag 1137

QY 1138 gtgacagagctgtgacagatgcgaaggaatggaacactttagtggtccagctcgg 1197

DB 379 gtgacagagctgtgacagatgcgaaggaatggaacactttagtggtccagctcgg 1197

QY 1198 aactgcacccaatctcagtgcaatgagtgatgtaattcccaaacactcttggaanaa 1257

DB 439 aactgcacccaatctcagtgcaatgagtgatgtaattcccaaacactcttggaanaa 1257

QY 1258 ttcatgctaacactacagagctatctacacgttccaaatggtgtaaaatggtgtaaa 498

DB 499 ttcatgctaacactacagagctatctacacgttccaaatggtgtaaaatggtgtaaa 498

QY 2074 gctggagcctcagggcgagccttgccagcaaacaccctgagggccagccttgctgc 2133
 Db 139 gctggagcctcagggcgagccttgccagcaaacaccctgagggccagccttgctgc 2133
 QY 2134 ccaagcgagcctcctctctcccgaggttgagcccgctcagtaagagttgggga 2193
 Db 139 ccaagcgagcctcctctctcccgaggttgagcccgctcagtaagagttgggga 2193
 QY 2194 agctcttcacttcggaggaattgctcaacaacatgctgggcatctgaccttact 2253
 Db 259 agctcttcacttcggaggaattgctcaacaacatgctgggcatctgaccttact 2253
 QY 2254 ctggtt 2258
 Db 319 ctggtt 323

RESULT 5
 AA288700
 ID AA288700 standard; DNA; 266 BP.
 AC AA288700;
 XX
 DT 11-MAY-2000 (first entry)
 DE Human CD95 receptor intron 1 fragment.
 XX
 KW p53; CD95 receptor; human; screening; apoptosis-modulation;
 KW cancer chemotherapy; ss.
 OS Homo sapiens.
 XX
 FH Key
 FT protein_bind Location/Qualifiers
 FT 160..179 /tag= a
 FT /bound_moiety= p53
 XX
 PN DE19847779-C1.
 XX
 PD 03-FEB-2000.
 XX
 PF 16-OCT-1998; 98DE-1047779.
 XX
 PR 16-OCT-1998; 98DE-1047779.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Krammer P, Mueller-Schilling M, Oren M;
 DR WPI; 2000-162245/15.
 XX
 PT Novel receptor DNA useful for identifying apoptosis-modulating
 PT substances potentially useful for cancer chemotherapy
 XX
 PS Claim 2; Fig 4; 12pp; German.
 XX
 CC This invention describes a novel p53-binding region of a human CD95
 CC receptor DNA molecule. The p53-binding region, or a vector containing
 CC it, can be used to screen for apoptosis-modulating substances
 CC potentially useful for cancer chemotherapy. This sequence represents a
 CC fragment of the human CD95 receptor intron 1 which contains a p53 binding
 CC region described in the method of the invention.
 XX
 SO Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;

Query Match
 Best Local Similarity 8.2%; Score 262.8; DB 21; Length 266;
 Matches 264; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2500 gatccgcctgggagggcgagcctcgcgctcctcctcgagacacactcgctcaggtt 2559
 Db 1 gatccgcctgggagggcgagcctcgcgctcctcctcgagacacactcgctcaggtt 60

QY 2560 gagctgggctgtggggcgagcaagaattgaagcgggaagctctgggaagcttaggtcgc 2619
 Db 61 gagctgggctgtggggcgagcaagaattgaagcgggaagctctgggaagcttaggtcgc 2619
 QY 2620 tggaggggagcccgcttggagagagagcgaacccctcggacaagccctgacagca 2679
 Db 121 tggaggggagcccgcttggagagagagcgaacccctcggacaagccctgacagca 2679
 QY 2680 gccaaaggtccgctccgagcggttggtgagtgccgcccgcggggcggggagga 2739
 Db 181 gccaaaggtccgctccgagcggttggtgagtgccgcccgcggggcggggagga 2739
 QY 2740 gagcctaacgcttcagacacatat 2765
 Db 241 gagcctaacgcttcagacacatat 266

RESULT 6
 AAC61798
 ID AAC61798 standard; DNA; 2551 BP.
 AC AAC61798;
 XX
 DT 06-MAR-2001 (first entry)
 DE DNA encoding a human Fas (Apo-1) protein.
 XX
 KW Human; Fas; Apo-1; antisense compound; Fas ligand; Fas-1; hepatitis;
 KW Fas associated protein 1; protein tyrosine phosphatase; cancer;
 KW autoimmune disease; inflammatory disease; lymphoma; ss.
 OS Homo sapiens.
 XX
 FH Key
 FT CDS Location/Qualifiers
 FT 221..1228 /tag= a
 FT /product= "Fas"
 XX
 PN WO200061150-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 10-APR-2000; 2000WO-US09540.
 XX
 PR 12-APR-1999; 99US-0290640.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Dean NM, Marcusson EG;
 DR WPI; 2000-628395/60.
 DR P-PSDB; AAB19341.
 XX
 PT Antisense oligonucleotides for treating hepatitis and colon, liver or
 PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
 PT 1 (Fas-1) expression
 XX
 PS Example 2; Page 71-73; 116pp; English.
 XX
 CC The present sequence encodes human Fas (Apo-1). The specification
 CC describes antisense compounds which are targeted to the 5'-untranslated
 CC region, translational start site, translational termination region
 CC or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
 CC ligand (FasL), or Fas-1 (Fas associated protein 1, protein tyrosine
 CC phosphatase). The antisense compounds are used to inhibit the
 CC expression of Fas, FasL or Fas-1 in cells or tissues. They are used
 CC to treat autoimmune or inflammatory diseases such as hepatitis. They
 CC can also be used to treat cancer, especially colon, liver or lung
 CC cancer or lymphoma.
 XX
 SO Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;

PT modulates FasL stimulation, used for treating graft versus host disease or autoimmune disease

PS Disclosure: Fig 4B; 71pp; English.

CC This present sequence is a DNA clone encoding soluble Fas receptor (see AAm98070). The invention provides a method for inhibiting a CC proinflammatory response in a cell mixture by administering a CC immunosuppressive agent which inhibits the proinflammatory activity of Fas ligand (FasL). In some embodiments, FasL is coadministered CC with the immunosuppressive agent, and the cell mixture comprises CC neutrophil cells. The method can be practiced in vitro, ex vivo or CC in vivo. Suitable immunosuppressive agents include antisense CC molecules that inhibit endogenous FasL expression, soluble Fas CC receptors, ribozymes that inhibit the endogenous expression of CC FasL, drugs that inhibit Fas signaling, agents that induce the CC and polynucleotides coding for an immunosuppressive agent such as CC TGF-beta. The method can be used for treating diseases associated CC with an undesired FasL-mediated proinflammatory response, e.g. CC graft versus host disease, or an autoimmune disease such as CC systemic lupus erythematosus, rheumatoid arthritis and psoriasis. CC The invention also provides a method for identifying agents which CC modulate FasL stimulation of a proinflammatory response.

SO Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;

Query Match
Best Local Similarity 7.0%; Score 226; DB 20; Length 2471;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2033 gacgctctgggagtgaggaagcggtttacagagtgactgtgagcctcagggcg 2092
DB 1 gacgctctgggagtgaggaagcggtttacagagtgactgtgagcctcagggcg 2092
QY 2093 ggcacgtgacgaggaacaccccttgagccagcctgctgcccagcgagctgctctt 2152
DB 61 ggcacgtgacgaggaacaccccttgagccagcctgctgcccagcgagctgctctt 2152
QY 2153 ctcccgcggtgtgtgagccgctcagtagaggttgaggagctcttcaactcggagg 2212
DB 121 ctcccgcggtgtgtgagccgctcagtagaggttgaggagctcttcaactcggagg 2212
QY 2213 atgtctcaacaacacatgctggcctctggaacctctcactctgtg 2258
DB 181 atgtctcaacaacacatgctggcctctggaacctctcactctgtg 2258

RESULT 9
AAQ29959
ID AAQ29959 standard; cDNA to mRNA; 2534 BP.

AC AAQ29959;
XX 12-MAR-1993 (first entry)
DE Human cell surface antigen.
XX Fas antigen; apoptosis; p58; NGFR/TNFR family; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 195..242 /*tag= a
FT mat_peptide 243..1199 /*tag= b
FT conflict 1046 /product= Fas_antigen
FT polyA_signal 1831..1836 /note= "this residue is not present in pF3"

FT polyA_signal /*tag= d
FT 2352..2357 /*tag= e
FT polyA_signal 2518..2523 /*tag= f

XX EP510691-A.
XX 28-OCT-1992.
XX 24-APR-1992; 92EP-0107060.
XX 26-APR-1991; 91JP-0125234.
XX (OSAB-) OSAKA BIOSCIENCE INST.

XX Itoh N, Nagata S, Yonehara S;
XX WPI: 1992-358914/44.
XX P-PSDB; AAR28084.

PT DNA encoding human cell surface antigen - used to clarify
PT apoptosis mechanism of various types of cell, and to prepare
PS monoclonal antibodies that react with tumour cells expressing Fas

PS Claim 3; Fig 1 and 2; 27pp; English.

CC A cDNA library was prepared from polyA+ RNA from the human lymphoma
CC cell line KT-3. The cDNA was ligated to BstXI-cut vector pCMT4 via
CC BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-
CC 7 cells which were then suspended in buffer containing murine anti-Fas
CC antibodies. The Fas-expressing cells adhered to the plates.
CC Extrachromosomal DNA was prepared from adhered cells and used to
CC transform E. coli W4100 cells. A 520bp XhoI-BamHI fragment from a
CC positive clone (pF3) was used to screen the KT-3 cDNA library. The
CC longest cDNA clone was designated pF58 and contains an ORF corresp.
CC (i.e. human Fas antigen).

SO Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match
Best Local Similarity 7.0%; Score 226; DB 13; Length 2534;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2033 gacgctctgggagtgaggaagcggtttacagagtgactgtgagcctcagggcg 2092
DB 1 gacgctctgggagtgaggaagcggtttacagagtgactgtgagcctcagggcg 2092
QY 2093 ggcacgtgacgaggaacaccccttgagccagcctgctgcccagcgagctgctctt 2152
DB 61 ggcacgtgacgaggaacaccccttgagccagcctgctgcccagcgagctgctctt 2152
QY 2153 ctcccgcggtgtgtgagccgctcagtagaggttgaggagctcttcaactcggagg 2212
DB 121 ctcccgcggtgtgtgagccgctcagtagaggttgaggagctcttcaactcggagg 2212
QY 2213 atgtctcaacaacacatgctggcctctggaacctctcactctgtg 2258
DB 181 atgtctcaacaacacatgctggcctctggaacctctcactctgtg 2258

RESULT 10
AAQ95297
ID AAQ95297 standard; cDNA; 2534 BP.

AC AAQ95297;
XX 19-FEB-1996 (first entry)
DE Plasmid pF58 contg. human Fas cDNA.

XX plasmid pF58; human Fas cDNA; soluble membrane protein;
 KW antibody production; diseases; treatment; prevention; ds.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS /tag= a
 FT 195..1202
 FT sig_peptide /tag= b
 FT 195..242
 FT mat_peptide /tag= c
 FT 243..1199
 FT
 FT JP07115988-A.
 PN
 XX 09-MAY-1995.
 PD
 XX 26-OCT-1993; 93JP-0267644.
 XX
 XX 26-OCT-1993; 93JP-0267644.
 PR
 XX (NIBS) JAPAN TOBACCO INC.
 PA
 XX WPI; 1995-202847/27.
 DR P-PSDB; AAR78606.
 XX
 XX Preparation of soluble membrane proteins - for their use in antibody
 PT production for the treatment and prevention of related diseases
 PS Example 1; Pages 15-17; 51pp; Japanese.
 CC AAG95297 is the plasmid pF58 which contains the human Fas cDNA. The
 CC plasmid was used in the construction of an expression vector for
 CC the prodn. of recombinant soluble membrane proteins. The proteins
 CC can be used in antibody prodn. for the treatment and prevention of
 CC related diseases.
 CC
 CC Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other:
 SQ
 Query Match 7.0%; Score 226; DB 16; Length 2534;
 Best Local Similarity 100.0%; Pred. NO. 1.5e-50;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2033 gacgctctcggagtgagggagcggttaccgagtgacttgctgagcctcagggcg 2092
 Db 1 gacgctctcggagtgagggagcggttaccgagtgacttgctgagcctcagggcg 60
 QY 2093 ggcactgacgagcaacacacccctgagcgagcctgctgcccagggcgagctcctt 2152
 Db 61 ggcactgacgagcaacacacccctgagcgagcctgctgcccagggcgagctcctt 120
 QY 2153 ctcccgcggtgtgtgagcccgctcagtaagagagttggggaagctcttcaactcggag 2212
 Db 121 ctcccgcggtgtgtgagcccgctcagtaagagagttggggaagctcttcaactcggag 180
 QY 2213 attgctcaacaacatgtggcagcttgagcctcctcactctgt 2258
 Db 181 attgctcaacaacatgtggcagcttgagcctcctcactcctgt 226
 RESULT 11
 AAT16303
 ID AAT16303 standard; cDNA; 2534 BP.
 XX
 XX AAT16303;
 AC
 XX 06-SEP-1996 (first entry)
 DT
 XX hfas coding sequence from plasmid pCEV4/hfas.
 DE
 XX Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
 KW

KW rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH CDS /tag= a
 FT 195..1201
 FT sig_peptide /product= Fas antigen
 FT 195..242
 FT mat_peptide /tag= b
 FT 243..1198
 FT /tag= c
 FT
 FT WO9601277-A1.
 PN
 XX 18-JAN-1996.
 PD
 XX 03-MAR-1995; 95NO-JP00349.
 XX
 XX 14-FEB-1995; 95JP-0025637.
 PR 06-JUL-1994; 94JP-0154706.
 XX
 XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
 PA (NIBS) JAPAN TOBACCO INC.
 XX Hachiya T, Noguchi J, Yonehara S;
 PI
 XX WPI; 1996-087635/09.
 DR P-PSDB; AAR92528.
 XX
 XX Immunoassay method for soluble Fas antigen in body fluids - for
 PT diagnosis of autoimmune diseases such as rheumatoid arthritis and
 PS systemic lupus erythematosus
 PT
 XX Example 8; Page 49-52; 124pp; Japanese.
 CC This sequence represents the coding sequence for the human Fas antigen
 CC contained within the plasmid pCEV4/hfas. The soluble Fas antigen is
 CC included in the immunoassay kit of the invention. The kit is for the
 CC assay of soluble Fas antigen and contains an immobilised anti-soluble Fas
 CC monoclonal antibody, as well as the standard soluble Fas antigen encoded
 CC by this sequence. The assay is simple and has high accuracy, high
 CC sensitivity, and is capable of assaying a number of different specimens
 CC at the same time. The immunoassay is used on biological samples (such as
 CC serum) and is useful for diagnosis of autoimmune diseases (such as
 CC rheumatoid arthritis or systemic lupus erythematosus (SLE)).
 CC
 CC Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other:
 SQ
 Query Match 7.0%; Score 226; DB 17; Length 2534;
 Best Local Similarity 100.0%; Pred. NO. 1.5e-50;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2033 gacgctctcggagtgagggagcggttaccgagtgacttgctgagcctcagggcg 2092
 Db 1 gacgctctcggagtgagggagcggttaccgagtgacttgctgagcctcagggcg 60
 QY 2093 ggcactgacgagcaacacacccctgagcgagcctgctgcccagggcgagctcctt 2152
 Db 61 ggcactgacgagcaacacacccctgagcgagcctgctgcccagggcgagctcctt 120
 QY 2153 ctcccgcggtgtgtgagcccgctcagtaagagagttggggaagctcttcaactcggag 2212
 Db 121 ctcccgcggtgtgtgagcccgctcagtaagagagttggggaagctcttcaactcggag 180
 QY 2213 attgctcaacaacatgtggcagcttgagcctcctcactcctgt 2258
 Db 181 attgctcaacaacatgtggcagcttgagcctcctcactcctgt 226
 RESULT 12
 AAV32993

ID AAV32993 standard; cDNA; 2534 BP.
 AC AAV32993;
 DI 18-NOV-1998 (first entry)
 DE Fas cDNA.
 KW Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;
 KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
 KW simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
 KW prophylactic; AIDS; ss.
 OS Mammalia sp.
 FA
 FH
 FT Key Location/Qualifiers
 FT CDS 195..1202
 FT sig_peptide /tag= a
 FT mat_peptide /tag= b
 FT polyA_signal /tag= c
 FT 1831..1836
 FT /*tag= d
 PN WO9835692-A1.
 PD 20-AUG-1998.
 PE 17-FEB-1998; 98WO-GB00485.
 PR 17-FEB-1997; 97GB-0003276.
 PX (ISIS-) ISIS INNOVATION LTD.
 PY Screation GR, Xu X;
 PI WPI: 1998-456867/39.
 DR P-PSDB; AAW49104.
 XX
 PT Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency
 PT diseases - by interfering with interaction of Fas with Fas-ligand
 PT expressed on activated CD4+ cells; e.g. cells infected with HIV
 PS Disclosure; Fig 10; 71pp; English.
 XX
 CC The present sequence represents a Fas cDNA sequence used in the
 CC method of the invention. The method is concerned with reducing
 CC depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)
 CC cells in an immune cell population which also comprises of Fas-ligand
 CC (FasL)-expressing activated CD4+ cells. It involves contacting this
 CC soluble Fas-Fc fusion protein which would interfere with the
 CC interaction between Fas and FasL. Therefore, the method is useful for
 CC identifying suitable agents which can reduce depletion of activated
 CC Fas-expressing CD8+ TK cells in immune cell populations. Also claimed
 CC is the use of the agent in the manufacture of therapeutic compositions.
 CC Apoptosis of lymphocytes can be triggered by the interaction of the
 CC cell surface receptor Fas and its ligand FasL. By interfering with
 CC this interaction, the method described and its preparations can prevent
 CC apoptosis of CD8+ TK lymphocytes caused by expression of FasL on
 CC activated CD4+ cells. Such FasL-expressing activated CD4+ cells are
 CC especially the result of CD4+ cell infection with an immunodeficiency
 CC virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency
 CC virus (SIV). The claimed prevention of apoptosis may then allow
 CC maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity
 CC towards the CD4+ cells infected with the infectious agent, enabling
 CC treatment (prophylactic and/or therapeutic) of immunodeficiency
 CC diseases e.g. AIDS.
 XX
 SQ Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match 7.0%; Score 226; DB 19; Length 2534;
 Best Local Similarity 100.0%; Pred. No. 1.5e-50;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2033 gaagctctggagagtgaggaagcgggtttacagtgactgtgagcctcagggcg 2092
 DB 1 gaagctctggagagtgaggaagcgggtttacagtgactgtgagcctcagggcg 60
 QY 2093 ggcactggcagcgaacacacccctgagcgcctggcgcctggcgcctggcgcct 2152
 DB 61 ggcactggcagcgaacacacccctgagcgcctggcgcctggcgcctggcgcct 120
 QY 2153 ctcccgaggtgtgtgagcccgctcagcagcaggttgggaagccttcacctcggag 2212
 DB 121 ctcccgaggtgtgtgagcccgctcagcagcaggttgggaagccttcacctcggag 180
 QY 2213 atgtctaacacacatctgtgacatctgagccctcactcctgtgt 2258
 DB 181 atgtctaacacacatctgtgacatctgagccctcactcctcgtgt 226
 RESULT 13
 AAV07002
 ID AAV07002 standard; cDNA to mRNA; 2534 BP.
 AC AAV07002;
 DI 16-JUL-1998 (first entry)
 DE Human Fas antigen cDNA.
 KW Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
 KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
 KW apoptosis modulation; ss.
 OS Homo sapiens.
 FA
 FH
 FT Key Location/Qualifiers
 FT CDS 195..1202
 FT sig_peptide /tag= a
 FT mat_peptide /tag= b
 FT 243..1199
 FT /*tag= c
 FT /product= Fas-antigen
 PN WO9742319-A1.
 PD 13-NOV-1997.
 PE 01-MAY-1997; 97WO-JP01502.
 PR 02-MAY-1996; 96JP-0135760.
 PX (MOCH) MOCHIDA PHARM CO LTD.
 PY (OSAB-) OSABA BIOSCIENCE INST.
 PI Nagata S, Nakamura N;
 DR WPI: 1997-558981/51.
 DR P-PSDB; AAW50289.
 XX
 PT Fas antigen derivative containing modified extracellular region -
 PT has low antigenicity, promotes apoptosis and is useful in treatment
 PT of viral and other diseases
 PS Disclosure; Fig 1-2; 102pp; Japanese.
 XX
 CC The present sequence was used in the development of novel Fas
 CC antigen derivatives, which contain a Fas antigen extracellular
 CC region lacking one or more amino acid residues in the region from
 CC the amino-terminal to (but excluding) the 1st cysteine residue

PT - targeting cytoplasmic and nuclear oncogene(s)
 XX
 PS Claim 1: Column 59-90; 92pp; English.
 XX

CC The present sequence represents an oncogene from the present invention.
 CC The present invention describes a composition which comprises two
 CC antisense oligonucleotides. The first oligonucleotide is specific for a
 CC cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1,
 CC c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and
 CC c-yes. The second oligonucleotide is specific for a nuclear oncogene or
 CC proto-oncogene selected from myc, jun, c-ets, c-fos, c-myc, B-myc,
 CC c-rel, c-vav, c-ski, c-spl, cyclin D1, PML/RAR alpha, AML1/MTG8,
 CC E2A/Prl and ALU-1/AF-4. The composition is used for treating cancer.
 CC The combination of antisense oligonucleotides has synergistically
 CC enhanced ability to inhibit growth of cancer cells.
 XX
 SQ Sequence 35100 BP; 8474 A; 8597 C; 9682 G; 8347 T; 0 other;

Query Match 1.9%; Score 59.8; DB 19; Length 35100;
 Best Local Similarity 55.6%; Pred. No. 0.00012;
 Matches 115; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
 QY 534 gaagatccacataatgtgagtgtgtatataatcacactcaagagatactgatttgt 593
 Db 3806 gaagtgacagtgagctgagatcatgcaactgacctccagcctagcgacagagaagact 593
 QY 594 caattgtccttccctcttcttctctctctctctctctctctctctctctctctctc 3865
 Db 3866 caatctccttc 653
 QY 654 tcccttctctccccaacaccccttctctctctctctctctctctctctctctctctc 3925
 Db 3926 ttccttc 713
 QY 714 actttcaatttggaaatagtttaga 740
 Db 3986 ttcttctcttc 3985
 3986 ttcttctcttc 4012

Search completed: September 7, 2002, 18:39:36
 Job time: 29870 sec

/lab_host="DH10B"
 /note="Vector: Bluescript SK; Site_1: EcoRI; Site_2: XhoI
 : This library was constructed by Kelian Tang, Robert
 Cole, and L. David Sibley at Washington University. cDNAs
 were synthesized from poly(A)+ RNA by Oligod(T) priming,
 size-selected and directionally cloned into the Uni-ZAP XR
 lambda vector (Stratagene). The primary library was mass
 excised as phagemids and rescued in SOLR cells. The
 plasmid library was recovered from the SOLR cells and
 transformed in mass into DH10B (GeneHog, Research Genetics
 , Inc.) for sequencing. WARNING: This library may contain
 a small percentage contaminants from human fibroblast
 cells."

BASE COUNT 86 a 191 c 140 g 89 t

ORIGIN

Query Match 100.0%; Score 125; DB 10; Length 506;
 Best Local Similarity 100.0%; Pred. No. 1e-19;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatccgcgtgagcagcgagcagctccgcgcctcctcgagacacacgtccacgtt 60
 |||||||
 Db 177 GATCCCGCTGGGCGAGCGGGCGGACCTCGGCGCTCTCGAGACACACCTCCACGCTT 118
 |||||||
 QY 61 gaggtggcgctggggggcgagcaggaattgaaagcgaaagcttgggaagctttagagtcgc 120
 |||||||
 Db 117 GAGGTGGCGCTGGGGCGGCGGACGAAATTAAGCGAAGCTCGGAGACCTTAGGCTGCC 58
 |||||||
 QY 121 tggag 125
 |||||
 Db 57 TGGAG 53

RESULT 2
 LOCUS AV695647 617 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV695647 GKC Homo sapiens cDNA clone GKCCD11 5', mRNA sequence.
 ACCESSION AV695647
 VERSION AV695647.1 GI:10297510
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 617)
 Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Hu, G., Gu, J., Chen, Z., and Han, Z., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 2165106
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

1. 617
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="GKCCD11"
 /clone_lib="GKC"
 /tissue_type="hepatocellular carcinoma"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: Bluescript sk(-); Site_1: EcoRI; Site_2:

BASE COUNT 122 a 210 c 179 g 104 t 2 others

ORIGIN

Query Match 100.0%; Score 125; DB 9; Length 617;
 Best Local Similarity 100.0%; Pred. No. 1e-19;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatccgcgtgagcagcgagcagctccgcgcctcctcgagacacacgtccacgtt 60
 |||||||
 Db 140 GATCCCGCTGGGCGAGCGGGCGGACCTCGGCGCTCTCGAGACACACCTCCACGCTT 81
 |||||||
 QY 61 gaggtggcgctggggggcgagcaggaattgaaagcgaaagcttgggaagctttagagtcgc 120
 |||||||
 Db 80 GAGGTGGCGCTGGGGCGGCGGACGAAATTAAGCGAAGCTCGGAGACCTTAGGCTGCC 21
 |||||||
 QY 121 tggag 125
 |||||
 Db 20 TGGAG 16

RESULT 3
 LOCUS AL540709 899 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL540709 LITL_FL002.PL1 Homo sapiens cDNA clone CS0DE002YN18 5 prime
 , mRNA sequence.
 ACCESSION AL540709
 VERSION AL540709.1 GI:12871113
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 899)
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1. 899
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DE002YN18"
 /clone_lib="LITL_FL002_PL1"
 /lab_host="DH10B"
 /note="Organ: Placenta; Vector: pCMVSPORT 6; 1st strand
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by life
 technologies. Contact : Feng Liang Life Technologies, a
 , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 192 a 288 c 245 g 170 t 4 others

ORIGIN

Query Match 100.0%; Score 125; DB 9; Length 899;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatccgcgtgagcagcgagcagctccgcgcctcctcgagacacacgtccacgtt 60
 |||||||
 Db 190 GATCCCGCTGGGCGAGCGGGCGGACCTCGGCGCTCTCGAGACACACCTCCACGCTT 131
 |||||||
 QY 61 gaggtggcgctggggggcgagcaggaattgaaagcgaaagcttgggaagctttagagtcgc 120
 |||||||

EST 25-SEP-2001

LOC630495	603049567f1
DEFINITION	NH_MGC_110
	mRNA sequence.
ACCESSION	B1763679
	GI:15755257

VERSION
KEYWORDS
SOURCE
ORGANISM

EST.
human.
Homo sapiens
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 793)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Robert Strausberg, Ph.D.

Comments: Email: cgapbs-remail.nih.gov
Tissue procurement: Life Technologies, Inc.
CNA Library Preparation: Life Technologies, Inc.
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Library Arrayed by: Incyte Genomics, Inc.
Sequencing by: Incyte Genomics, Inc.
Sequencing information can be found at: <http://www.genome.gov>

Clone identifier found through the I.M.A.G.E. Consortium/[llnl.gov](http://image.llnl.gov)
<http://image.llnl.gov>
 Plate: LLAM11474 row: e column: 17
 High quality sequence stop: 786.
 Qualifiers

```

SOURCE
1. '93
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGP:5189752"
/clone_1ib="N1H_MGC_116"

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12-13-14-15-16-17-18-19-20-21-22-23-24-25-26-27-28-29-30-31-32-33-34-35-36-37-38-39-40-41-42-43-44-45-46-47-48-49-50-51-52-53-54-55-56-57-58-59-60-61-62-63-64-65-66-67-68-69-70-71-72-73-74-75-76-77-78-79-80-81-82-83-84-85-86-87-88-89-90-91-92-93-94-95-96-97-98-99-100-101-102-103-104-105-106-107-108-109-110-111-112-113-114-115-116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000-1001-1002-1003-1004-1005-1006-1007-1008-1009-1010-1011-1012-1013-1014-1015-1016-1017-1018-1019-1020-1021-1022-1023-1024-1025-1026-1027-1028-1029-1030-1031-1032-1033-1034-1035-1036-1037-1038-1039-1040-1041-1042-1043-1044-1045-

Oligo-dT primed cDNA was ligated into BamHI-digested pUC19 destroyed upon cloning). Library is normalized and insert size range 1-3 kb. Library was constructed by inserting full-length clones and was constructed by enriched for full-length clones and was constructed by Research Genetics tracking code Gruber (Invitrogen), "with MC library."

BASE COUNT	ORIGIN
183 a	265 c
208 g	137 c

67.49. SCORE 121.8; DB 10; Length 793;

[illegible][illegible]

Qy	1.21	tgag	1.25
D _b	4.37	TGAG	4.33

RESULT	LOCUS	DEFINITION
BG121079/c	1140 bp	mRNA
BG121070		linear
EST:50-04		EST:4451039
LOCUS	602352793F1	NIH_MGC_90 Homo sapiens CDNA clone IMAGE:4451039
DEFINITION		mRNA sequence.

VERSION	BGL2107.0.1	DATE
KEYWORDS	EST.	
SOURCE	human.	

1

Homo sapiens
Filkaruot

cyprus@lethal.nih.gov
Tissue Procurement: ATCC

FEATURES
source

BASE COUNT
ORIGIN

Query Match	Best Local Similarity	Score	DB ID	Length
Matches 123; Conservative	88.6%; 97.6%;	110.8;	DB 10;	1140;
			Mismatches 2;	Indels 1;
QY 1 gatccgcctctggagcggcgagctccgcgctcctcgagacacatcgctcccaagt				
DB 163 GACCCCGCTGGGCAAGCGGGGAGCTCCGGGCTCTCGAACAACATCCCTCCACGTT				
QY 61 gaggttgagcgttgaggcgagacaggaattgaacggaagt-ctgggaagcrtttagggctcg				
DB 103 GAGGTGGGCGTGGGTGGGACAGCAAGAAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCG				
QY 120 ctggag 125				
DB 43 CTGGAG 38				

RESULT	7
AV692383/c	
LOCUS	
DEFINITION	AV692383 GKC Homo sapiens 359 bp mRNA
ACCESSION	AV692383
VERSION	AV692383
KEYWORDS	AV692383.1 GI:10294246
SOURCE	EST.
ORGANISM	human.
	Homo sapiens
	linear EST 16-JAN-2002
	c1one GKCcMG5 5', mRNA sequence.

REFERENCE	AUTHORS
1 (bases 1 to 359)	Primates; Catarrhini; Hominae; Homo.
Xu, X., Huang, T.	Primates; Catarrhini; Hominae; Homo.

TITLE

JOURNAL OF HEPATOLOGY
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE 21625106
COMMENT Contact:

Contact: Zengqiang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922

Location/Qualifiers
1. .359

BASE COUNT	ORIGIN	57 a	148 c	98 g	55 t	others
ecori; site_2						1

Query Match	87.2%;	Score 109;	DB 9;	Length 359;
Best Local Similarity	100.0%;	Pred. No.	5.2e-16;	
Matches 109;	Conservative			

[illegible]

RESULT	8		
BI463384			
LOCUS	BI463384	800 bp	mRNA
DEFINITION	603004413F1 NTH_MGC_97	Homo sapiens	CDNA clone
ACCESSION	BI463384		IMAGE:5270114 5',
VERSION	BI463384.1	GI:15254040	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		

REFERENCE AUTHORS TITLE JOURNAL COMMENT	REFERENCE AUTHORS TITLE JOURNAL COMMENT
NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Unpublished (1999) Contact: Robert Stevens	Primates; Catarrhini; Strepsirrhini; Eulestomidae; Hominoidea; Homo. Mammalian Gene Collection (MGC)

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ULNL at:
<http://image.llnl.gov>
 Plate: LRAM1681 row: j column: 03
 High quality sequence stop: 731.
 Location/Qualifiers
 1..800

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/organ="testis"; Vector: pBluescript (modified
/lab.host="DH10B"
/clone.lib="NIH_MGC_97"
/clone="IMAGE:5270114"
/db_xref="taxon:9606"
/db_xref="homol_sapiens"
/organ="testis"; Vector: pBluescript (modified

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OY 1 gatccgcgtggcagcgagcgagcagctccgcgcctcctcggagagaccactgctccacgtt 60
 Db 461 GCTTCCACCGGGCTTGAACCAACAGGAGGAGCTCCGCTTAAGACTCCACCCCGCTG 520
 OY 61 gaggctggcgctgggggagcgagcaggaattgaagcgaagtctctgggaagc 109
 Db 521 GGGGTGGGGGGGGGTGCTCCGCGGAATGAAATGAGATGAGCCCGAGGAGCC 569

RESULT 11
 A1623104 333 bp mRNA linear EST 15-DEC-1999
 A1623104/c
 LOCUS
 DEFINITION tu49f10.x1 NCI-CGAP_P128 Homo sapiens CDNA clone IMAGE:2254411 3',
 mRNA sequence.
 ACCESSION A1623104
 VERSION A1623104.1 GI:4648029
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominiina; Homidae; Homo.
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 COMMENT Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apb-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.lnl.gov/dbp/ncicgap/ncicgap.html
 Insert Length: 397 Std Error: 0.00
 Seq primer: -40UP from Glibco
 High quality sequence stop: 321
 POLYA-NO.

FEATURES
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 1..333
 /location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:2254411"
 /clone_1b="NCI-CGAP_P128"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker. Plasmid DNA from the
 normalized library NCI-CGAP_P122 was prepared, and as
 this DNA was made in vitro. Following HAP purification,
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 1101192-1101959, and 1217928-1220615).
 Subtraction by Bento Soares and M. Fatima Bonaldo."
 78 a 111 c 88 g 56 t

BASE COUNT

ORIGIN

Query Match 29.3%; Score 36.6; DB 9; Length 333;
 Best Local Similarity 58.9%; Pred. No. 37;
 Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

OY 3 tccgcgtggcagcgagcgagcagctccgcgcctcctcggagagaccactgctccacgtt 62
 Db 225 TTCCACCGGGCTTGAACCAACAGGAGGAGCTCCGCTTAAGACTCCACCCCGCTG 166
 OY 63 ggtggcgctgggggagcgagcaggaattgaagcgaagtctctgggaagc 109
 Db 171 GGTGGGGGGGGGTGCTCCGCGGAATGAAATGAGATGAGCCCGAGGAGCC 125

Db 165 GGTGGGGGGGGGTGCTCCGCGGAATGAAATGAGATGAGCCCGAGGAGCC 119

RESULT 12
 A1393907 392 bp mRNA linear EST 30-MAR-1999
 A1393907/c
 LOCUS
 DEFINITION tg05f09.x1 NCI-CGAP_CLL1 Homo sapiens CDNA clone IMAGE:2107913 3',
 mRNA sequence.
 ACCESSION A1393907
 VERSION A1393907.1 GI:4223454
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominiina; Homidae; Homo.
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 COMMENT Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apb-remail.nih.gov
 Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
 M.D., Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.lnl.gov/dbp/ncicgap/ncicgap.html
 Insert Length: 746 Std Error: 0.00
 Seq primer: -40UP from Glibco
 High quality sequence stop: 383.

FEATURES

source

1..392
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 /db_xref="taxon:9606"
 /clone="IMAGE:2107913"
 /clone_1b="NCI-CGAP_CLL1"
 /tissue_type="B-cell, chronic lymphocytic leukemia"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTACCAATCTGAGTGAAGGAGGAGGCGGCGATTCCTCTTTTCTTTTCTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and Eco RI
 the Not I and Eco RI sites of the modified pT73 vector.
 Library is normalized, and was constructed by Bento
 Soares and M. Fatima Bonaldo."
 92 a 128 c 101 g 71 t

BASE COUNT

ORIGIN

Query Match 29.3%; Score 36.6; DB 9; Length 392;
 Best Local Similarity 58.9%; Pred. No. 37;
 Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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 Db 231 TTCCACCGGGCTTGAACCAACAGGAGGAGCTCCGCTTAAGACTCCACCCCGCTG 172
 OY 63 ggtggcgctgggggagcgagcaggaattgaagcgaagtctctgggaagc 109
 Db 171 GGTGGGGGGGGGTGCTCCGCGGAATGAAATGAGATGAGCCCGAGGAGCC 125

RESULT 13

BE908413 426 bp mRNA linear EST 20-OCT-2000
 BE908413
 LOCUS
 DEFINITION 601503040F1 NIH_MGC_70 Homo sapiens CDNA clone IMAGE:3905120 5',
 mRNA sequence.
 ACCESSION BE908413

TGTTACCAATCTGAGTGGAGCGCCGACATGCTTTT
 T 3,1; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified p7773 vector.
 Library is normalized, and was constructed by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 104 a 137 c 119 g 72 t
 ORIGIN

Query Match 29.3%; Score 36.6; DB 9; Length 432;
 Best Local Similarity 58.9%; Pred. No. 39;
 Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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 QY 63 ggtggcgctggggcgagcaggaattgaagcgaagctcgggaagc 109
 Db 163 GGTGGGGCGGGTGTCCGTCCGAAATGAAGGAATAGCCCGAGAGACC 117

Search completed: September 7, 2002, 14:51:36
 Job time: 16195 sec

[illegible]

RESULT	8
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DEFINITION	Human DNA sequence from clone RP11-399019 on chromosome 10,
ACCESSION	complete sequence.
VERSION	AL157394
KEYWORDS	HTG.
SOURCE	GI:15384622
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	Blakey S. Direct Submission
JOURNAL	Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
COMMENT	CBI015A, UK. E-mail enquiries: humquerry@sanger.ac.uk On Aug 31: clonerequest@sanger; humquerry@sanger.ac.uk

Requests: clonerequest@sanger.ac.uk; humquery@sanger.ac.uk
On Aug 31, 2001, this sequence version replaced gi:14161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations.
Together with a note of the overlapping clones.
variation annotation may not be found in the sequence.
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted:
Regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30): an attempt was made to resolve all sequencing problems, such
as one plasmid subclone and repeats; all regions were covered by at
least one subclone or more than one M13 subclone; and the
abbreviations are used to associate primary digest. The following
in the feature table with their source databases: Em: EMBL; S: S;
SWISSPROT: Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C-elegans/Wormpep
This sequence was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGC/Chr10
R313-39019 is from the library RPC1-11.2 constructed by the group
of Pleter de Jong. For further details see

gatccgcgtgqcaaacacccccct	36; Indels	0; Gaps
--------------------------	------------	---------

.....GAGCGCCACGATYGAAGCGAA 193

ORGANISM Homo sapiens Eukaryota

Isolation of a cDNA which corrects chromosome breakage in Fanconi anemia cells

1. .1269
/Organism-Bu

223

N	C	g	t
	413	263	

3
+
+
+
+

874 TTCACCGG

934 GCTCCGCGC

12

REFERENCE

TITL E

JOURNAL

source

1

100

4262 TPC

4322 CCM

SULT 13

WORDS 510

Euk.

White

Geno
9607

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RESULT 14
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 DEFINITION
 ACCESSION Y14385.1 GI:2653423
 VERSION inositol polyphosphate 5-phosphatase; SHIP2 gene.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 4743)
 AUTHORS Pesesse, X., Delen, S., De Smedt, F., Drayer, L., and Erneux, C.
 TITLE Identification of a second SH2-domain-containing protein closely
 related to the phosphatidylinositol polyphosphate 5-phosphatase
 SHIP
 JOURNAL Biochem. Biophys. Res. Commun. 239 (3), 697-700 (1997)
 MEDLINE 98042455
 REFERENCE 2 (bases 1 to 4743)
 AUTHORS Pesesse, X.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUL-1997) X. Pesesse, Interdisciplinary Research
 Institute, Université Libre de Bruxelles, Campus Erasme Bldg. C,
 808 Route de lennik, 1070 Brussels, BELGIUM

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 Matches 63; Conservative 0; Mismatches 44;
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 Oy 63 gttggcgctgtggcgagcgagcgtccgcgtccgcagaccatgcgtccagctga 109
 4408 GGTGGGGGGGCTGCTCCGTAAGAGATGAGCCGAGGACC 4454

RESULT 15
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 DEFINITION
 ACCESSION AP000593.4 GI:17425220
 VERSION HTG.
 KEYWORDS
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 124635)
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (12-OCT-1999) Masahiro Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
 1-7-22 Suenho-chou, Tsukuba, Ibaraki, 305-3858, Japan
 (E-mail:hattori@gs.c.riken.go.jp, URL:http://hgc.gsc.riken.go.jp/,
 tel:81-45-503-9111, Fax:81-45-503-9170)
 On Dec 7, 2001 this sequence version replaced gi:12246850.
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us-09-834-291-2_copy_1_125.rge

Page 8

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Matches 63; Conservative	0;	Mismatches 44.		

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QY 63	gctggcgtgggggcgcgaacgaattgaacgcggaagctcggaaagc	109	
Db 27633	GGTGGGGCGGCTCTCCCTCCGGAATGTAAGGAATAGCCCGAGGACC	27679	

Search completed: September 7, 2002, 18:26:54
Job time: 29113 sec

Mon Sep 9 09:30:39 2002

GenCore version 4.5
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Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: September 7, 2002, 18:30:49 ; Search time 12179.2 seconds
(without alignments) updates/sec 4857.402 Million cell

Title: US-09-834-291-4
Perfect score: 2827
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Scoring table: IDENTITY NUC
Gapop 10.0, Capext 1.0
1797656 seqs, 10463268293 residues
3595312

Searched: Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenEmbl:
1: gb_da:*
2: gb_hg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
7: gb_ov:*
8: gb_ov:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score distribution.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

us-09-834-291-4.rge

1 2827 100.0 2827 6 AX026092
2 2380 84.2 2380 6 AX026091
3 2365.6 83.7 187313 6 AX157394
4 2346.6 83.0 3212 6 AX026089
5 2162 76.5 2344 9 HSDP955FR
6 1714.4 60.2 1877 9 HSDP955FR
7 1702.4 48.6 1608 6 HSDP955FR
8 1372.8 31.1 1608 6 AX347320
9 879.4 30.3 1608 6 AX026090
10 611.8 21.6 398 11 G27038
11 259 9.2 2719 9 BC012479
12 245 8.7 702 9 HSA279012
13 216 7.6 702 9 HSA279012
14 216 7.6 702 9 HSA279013
15 216 7.6 702 9 HSA279013
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ALIGNMENTS

RESULT 1
AX026092 2827 bp DNA
LOCUS AX026092 4 from patent DE19847779.
DEFINITION AX026092
ACCESSION AX026092.1 GI:10187523
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2827)
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
TITLE Novel receptor the useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL DEUTSCHES KREBSFORSCH (DE)
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DB	1	tsagagctctagaatctgctgtgtaataataaataaactcttagagatgccaactgtc			
QY	61	ttcccccagaacacccagcaltcattaggtgtcaltcgaatagatcttccaagatcca			
DB	61	ttcccccagaacacccagcaltcattaggtgtcaltcgaatagatcttccaagatcca			
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DB	241	ctgaagatcttgacacatgaacataatgctcccccagaagaacatcttctctctc			
QY	301	gaacttggagataattgagctacgtgggtagaaggttaggggaaggggtatgcataga			
DB	301	gaacttggagataattgagctacgtgggtagaaggttaggggaaggggtatgcataga			
QY	361	aaagagcagagccttggggaacagaataatcctaagcttaactcctgactctgactatata			
DB	361	aaagagcagagccttggggaacagaataatcctaagcttaactcctgactctgactatata			
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DB	721	atttggaaatagtttagaatttcaaaaaatttgcagaagaataaagaagaatgccaata			
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DB	781	tacacatccctcctcactcacttcttctgtctcattagatcctaaggtgtgtgcaaa			
QY	841	ggcttggagcccccagggcttctcctcagcactaacaagctgaaggttgaagaag			
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DB	901	acaagcctcacaac			
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DB	1441	gcttaagtgcttgaatgttctcctcctcctcctcctcctcctcctcctcctcctcctc			
QY	1501	cagagccctatgagcagaacatcctgactcttctcataatgataatgataatgataatgata			
DB	1501	cagagccctatgagcagaacatcctgactcttctcataatgataatgataatgataatgata			
QY	1561	gtctgtgaagcctcactgcttgcagcagaacatgagaaccccaagtcacagcagaa			
DB	1561	gtctgtgaagcctcactgcttgcagcagaacatgagaaccccaagtcacagcagaa			
QY	1621	tccttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc			
DB	1621	tccttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc			
QY	1681	gcttgaagcctcactgcttgcagcagaacatgagaaccccaagtcacagcagaa			
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OY

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FEATURES

Location/Qualifiers

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KEYWORDS	HTG.		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	Blakey, S.		
JOURNAL	Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,		
COMMENT	CH10 15A, UK. E-mail enquiries: humquerry@sanger.ac.uk		
	requests: clonerequest@sanger.ac.uk		
	On Aug 31, 2001 this sequence version replaced gi:14161146.		
	During sequence assembly data is compared from overlapping clones.		
	Where differences are found these are annotated as variations		
	corresponding to a note of the overlapping clone name. Note that the		
	only a small overlap as described above.		
	This sequence was finished as follows unless otherwise noted: all		
	regions were either double-stranded or sequenced with an alternate		
	chemistry or covered by high quality data (i.e., phred quality >=		
	30); an attempt was made to resolve all sequencing problems, such		
	as compressions and repeats; all regions were covered by at least		
	one plasmid subclone or more than one M13 subclone; and the		
	abbreviations are used to associate primary accession numbers given		
	in the feature table with their source databases: Em.; EMBL; SW.;		
	SWISSPROT; Tr.; TrEMBL; WPI.; WORMPEP; Information on the WORMPEP		
	database can be found at		
	http://www.sanger.ac.uk/projects/C_elegans/wormpep		
	was generated from part of bacterial clone contigs of human		
	chromosome 10, constructed by the Sanger Centre Chromosome 10		
	Mapping Group. Further information can be found at		
	http://www.sanger.ac.uk/HGP/Chr10		
	of P1er de Jong. Is from the library RPCT-11.2 constructed by the group		
	http://www.chori.org/bacpac/home.htm		
	VECTOR: pBACE3.6		
	This sequence is the entire insert of clone RP11-399019 The true		
	left end of clone RP11-496H23 is at 166408 in this sequence. The		
	true right end of clone RP11-30415 is at 18704 in this sequence.		

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DB 238	aagcgcaagaagatttgggggaacagatataataattaccacaccccttgaacatagac	180		
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 Wada, N., Matsumura, M., Ohba, Y., Kobayashi, N., Takizawa, T. and
 Nakanishi, Y.
 1 (bases 1 to 2165)
 transcripion stimulation of the Fas-encoding gene by nuclear
 factor for interleukin-6 expression upon influenza virus infection
 J. Biol. Chem. 270 (30), 18007-18012 (1995)
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 JOURNAL 2 (bases 1 to 2165)
 Nakanishi, Y.
 Direct Submission
 Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University,
 Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa,
 Ishikawa 920-0934, Japan (E-mail: nakanaka@ds.p.kanazawa-u.ac.jp,
 Tel: 076-234-4424, Fax: 076-234-4480)
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RESULT 8
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VERSION X82279.1
KEYWORDS GI:673405
SOURCE Apo-1 gene, Fas gene.
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Cheng, J., Liu, C., Koopman, W.J., and Mountz, J.D.
TITLE Characterization of human Fas gene. Exon/intron organization and
JOURNAL J. Immunol. 154 (3), 1239-1245 (1995)
MEDLINE 95123075
REFERENCE 2 (bases 1 to 1608)
AUTHORS Cheng, J.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1994) J. Cheng, Univ. of Alabama at Birmingham, Birmingham, AL 35294-0007, USA
COMMENT Related sequences: M67454 and X63717.
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REFERENCE 1 (sites)
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 020928-A 2392 03-Jan-2002.
Epidemiol. Infect.
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Direct access.

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H-MGC Project URL: <http://mga.gs.washington.edu>
 Contact: MGC help desk
 Email: cganb@u.washington.edu

Procurement: ATCC
Library Preparation: ATCC
Sequencing Array: ATCC

ATCC-20892-2590,
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Technology, Inc.
The I.M.A.G.E. Consortium
Baylor College of Medicine
Baylor Research Center
site: <http://bcm-hgsc>

Human Genome

distribution: MGC clone
the I.M.A.G. B.

Hulk, S., Lu, X., Garcia

B, Hodgson, A., Bouck, J.

Consortium/LLNL at: <http://image>

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Page 16

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M., Reid
Catarrh

Mutations of the CD95 gene affect of the germinal center

Huganickel, B., Diehl, V., Rajewsky

Hominidae; Euteleostomi; Homioidea; Homo.

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Mon Sep 9 09:30:39 2002

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Job time: 29633 sec

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Mon Sep 9 09:30:41 2002

us-09-834-291-4.rml

GenCore version 4.5
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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
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Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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2	129	4.6	2471	US-08-444-231-18	Sequence 18, Appl
3	129	4.6	2471	US-08-152-443A-18	Sequence 18, Appl
4	129	4.6	2534	US-08-219-237B-1	Sequence 1, Appl
5	129	4.6	2534	US-08-468-560C-1	Sequence 16, Appl
6	129	4.6	2534	US-09-180-100-16	Sequence 14, Appl
7	79.4	2.8	7218	US-08-232-463-14	Sequence 10, Appl
8	67.4	2.4	7218	US-08-836-022A-10	Sequence 10, Appl
9	63.6	2.2	19307	US-09-427-048A-10	Sequence 3, Appl
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11	62.6	2.2	9972	US-09-427-048A-3	Sequence 2, Appl
12	62.6	2.2	4476	US-08-801-344-2	Sequence 2, Appl
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14	62.4	2.2	35100	US-08-306-691B-19	Sequence 19, Appl
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16	59.8	2.1	35100	US-09-018-584A-25	Sequence 8, Appl
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18	50.8	1.8	370	US-08-623-906A-18	Sequence 7, Appl
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21	49.2	1.7	361	US-09-018-557B-35	Sequence 35, Appl
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23	48.4	1.7	15144	US-08-458-434A-6	Sequence 24, Appl
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43	47.2	1.7	434	2	US-08-332-766A-10	Sequence 19, Appl
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ALIGNMENTS

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Sequence 1, Appl
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (221)..(1228)
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 267
ISSUE: 15
PAGES: 10709-10715
DATE: 1992-05-25
DATABASE ACCESSION NUMBER: X63717/Genbank
DATABASE ENTRY DATE: 1996-07-19
US-09-290-640-1

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RESULT 2
US-08-444-231-18

Sequence 18, Application US/08444231
Patent No. 5652210

GENERAL INFORMATION:

APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES: 22
ADDRESS: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,231
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 530
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS
LOCATION: 195..1136
FEATURE: 195..1136
NAME/KEY: mat_peptide
LOCATION: 243

US-08-444-231-18

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Sequence 18, Application US/08152443A
Patent No. 5663070
GENERAL INFORMATION:

Mon Sep 9 09:30:41 2002

us-09-834-291-4.rml

ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516762
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
ORIGINAL SOURCE: CDNA to mRNA
ORGANISM: Homo sapiens
IMMEDIATE SOURCE: LIBRARY: PCEV4
CLONE: clone pF58

FEATURE: CDS
NAME/KEY: 195..1202
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: sig_peptide
NAME/KEY: 195..242
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: mat_peptide
NAME/KEY: 243..1199
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 1831..1836
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: sig_peptide
NAME/KEY: 2352..2357
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: mat_peptide
NAME/KEY: 243..1199
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 2518..2523
LOCATION: 2518..2523
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 2352..2357
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
US-08-219-237B-1

Query Match 4.6%; Score 129; DB 2; Length 2534;
Best Local Similarity 100.0%; Pred. No. 2; 3e-26; Indels 0; Gaps 0;
Matches 129; Conservative 0; Mismatches 0;
2034 gacgctctgagtgaggagcggttaacagtgactgctgagcgccacagggcg 2093

Db 1 GACGCTCTGGAGACTGAGGAGCCGTTTACAGTGACTGTGCTGAGCCTCAGGCGG 60
Gy 2094 ggaactgacaggaacacacccctagggcagccctgctgccccagcgagctgctctt 2153
Db 61 GGCACCTGCACGACACACCTTGTAGGAGCAGCCTGCTGCTCCAGGCGGAGCTGCTCTT 120
Gy 2154 ctccgcgcg 2162
Db 121 CTCCGCGCG 129

RESULT 5
US-08-468-560C-1
Sequence 1, Application US/08468560C
Patent No. 6270998
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
ORIGINAL SOURCE: CDNA to mRNA
ORGANISM: Homo sapiens

FEATURE: CDS
NAME/KEY: 195..1202
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: sig_peptide
NAME/KEY: 195..242
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: mat_peptide
NAME/KEY: 243..1199
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 1831..1836
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: sig_peptide
NAME/KEY: 2352..2357
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus
FEATURE: polyA_site
NAME/KEY: 2518..2523
LOCATION: 2518..2523
IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus


```

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-f1s
US-08-232-463-14

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Query Match 2.4%; Score 67.4; DB 1; Length 7218;
Best Local Similarity 8.0%; Pred. No. 1.2e-08;
Matches 35; Conservative 228; Mismatches 174; Indels 0; Gaps 0;

QY 807 ttgtctattagatgctcagagtggtgacaaagctgcacgcccagggcttcctca 866
DB 1442 TTGTGTAACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1383
QY 867 tggcactaacgtctactgaaggtgacagagaacagcctatcaacactacaagact 926
DB 1382 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1323
QY 927 ggtgtaagtcagtcagacagacagacagagtgatgacagcctcagagaggtaa 986
DB 1322 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1263
QY 987 cctaactgattgagggcccaaacagctccagaagaagtgcacactgagagaagc 1046
DB 1262 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1203
QY 1047 ctgaagatgacagcgggtgacaaaggtatataatgttataatggtgtaac 1106
DB 1202 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1143
QY 1107 taatgggaagagagaggtgacagagtgatgacagagctggtgagacatgccaag 1166
DB 1142 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1083

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QY 1167 gaatactgaacctttagtgtgctcagtcggaactgcatccaattcagttcagta 1226
DB 1082 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1023
QY 1227 gatgcatatccaac 1243
DB 1022 GTGAGCCTATGCGCAAC 1006

```

```

RESULT 9
US-08-836-022A-10
Sequence 10, Application US/08836022A
Patent No. 6001557
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
APPLICANT: Wilson, James M.
APPLICANT: Fisher, Krishna J.
APPLICANT: Chen, Shu-Jen
APPLICANT: Weltman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-5818
TELEFAX: 215-540-9200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
US-08-836-022A-10

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Query Match 2.2%; Score 63.6; DB 3; Length 19307;
Best Local Similarity 65.5%; Pred. No. 2.7e-07;
Matches 93; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2114 cctgaagcagccctgtgctgcccagcgaggtcctctcccgcgagacatgtacaga 2173
DB 16048 CGCGCGCGCTCAGCTGCGCCATCGATACGCTACGCGGACCGCGCATGTACGA 16107
QY 2174 gctgagaagtaactgtgacacgtgagcgtgtgacacttaagcttgggtcgctgag 2233
DB 16108 GCTGAGAAGTACTGTGTGCGCACGTTGCGCGCGCTTAAGCTTGGCCTGCGCTGCT 16167
QY 2234 gggaccccggttgagagagga 2255
DB 16168 TTTACAACGTCGTAAGTGGAA 16189

```


NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION/DOCKET NUMBER: GNVFN, 008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-427-048A-3

Query Match 2.2%; Score 62.6; DB 4; Length 9972;
Best Local Similarity 65.2%; Pred. No. 3.4e-07;
Matches 92; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 2115 ctgagagccagccctgctgcccagcgagagctgctcttcctccgagacatgtacagag 2174
DB 2980 CGGCCCGCTGCGACGCTGCGCCATCGATGCGCTGCGCGCGCGGACATGTACAGAG 2921
QY 2175 ctgagagagctagctgagcagctgagcgctgacacttaagcttaagctgagcgagag 2234
DB 2920 CTCGAGAGTACTAGTGGCCGCGCTGCGCGCTGACCTTAAGCTTGGCACTGCGCTGTT 2861
QY 2235 ggaacccggttgagagagga 2255
DB 2860 TTACAACGTCTGACTGGAA 2840

RESULT 13
US-08-801-344-2
Sequence 2, Application US/08801344
Patent No. 6087140
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL
TITLE OF INVENTION: FROM SUGAR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demilt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: U.S.A.
ZIP: 53717-1914

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,344
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Vector pSE380

US-08-801-344-2
Query Match 2.2%; Score 62.4; DB 3; Length 4476;
Best Local Similarity 75.0%; Pred. No. 2.3e-07;
Matches 78; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 2115 ctgagagccagccctgctgcccagcgagagctgctcttcctccgagacatgtacagag 2174
DB 523 CGGCCCGCTGCGACGCTGCGCCATCGATGCGCTGCGCGCGGACATGTACAGAG 582
QY 2175 ctgagagagctagctgagcagctgagcgctgacacttaagcttaagctgagcgagag 2218
DB 583 CTCGAGAGTACTAGTGGCCGCGCTGCGCGCTGACCTTAAGCTT 626

RESULT 14
US-09-498-599-2
Sequence 2, Application US/09498599
Patent No. 630352
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL FROM SUGAR
TITLE OF INVENTION: 1,2-PROPANEDIOL FROM SUGAR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demilt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,599
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Vector pSR380
US-09-498-399-2

Query Match
Best Local Similarity 2.2%; Score 62.4; DB 4; Length 4476;
Matches 78; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 2115 ctgaagcagccctgctgcccagcgagctcctctctcccgcgagatgtagag 2174
DB 523 CGGCCGCTGACGTCGCCATCGATCGCTACGTCGCCGCGACGACATGTACAGAG 582
QY 2175 ctgaagagactagtagcgagctgagccgctgacacctaagctt 2218
DB 583 CTCGAGAGTACTACTGCGCAGCTGGCCGCTGACCTTAACCTT 626

RESULT 15
US-08-306-691B-19
Sequence 19 Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavoraga & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-306-691B-19

Query Match
Best Local Similarity 2.1%; Score 59.8; DB 1; Length 35100;
Matches 115; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
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DB 3806 GAGGTTCAGTACGTCGATGATCATCCACTGACCTCAGCCTAGCCACAGACGAC 593
QY 594 caattgctccctccctctctctctctctctctccctccctccctccctcc 3865
DB 3866 CCATCTCCT 653
QY 654 tcccttccctccctccacaccccttccctccctctctctctctctctctct 3925
DB 3926 TTCCTTCT 713
QY 714 acttccatttggaatagtttaagga 740
DB 3986 TTCCTTCT 3985

Search completed: September 7, 2002, 18:29:19
Job time: 29253 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
September 7, 2002, 18:41:53 : Search time 1139.19 Seconds
(without alignments)
4260.674 Million cell updates/sec

Run on: US-09-834-291-4
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Title: 2827
Perfect score: 1
Sequence: IDENTITY NUC
Scoring table: Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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22: /SIDSL/gcgdata/hold-genesec/genesecq-emb1/NA2001B.DAT: *
23: /SIDSL/gcgdata/hold-genesec/genesecq-emb1/NA2002.DAT: *
24: /SIDSL/gcgdata/hold-genesec/genesecq-emb1/NA2002.DAT: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1372.8	48.6	1608	17	AAAT34162
2	879.4	31.1	1608	24	ABL34419
3	856.8	30.3	1608	24	ABL34418
4	190.4	6.7	859	21	AAAC96177
5	161	5.7	266	21	AAZ88700
6	155	5.5	2551	21	AAAC61798
7	129	4.6	2471	16	AAAC93879
8	129	4.6	2471	20	AAAX24878
9	129	4.6	2534	13	AAO29959

ALIGNMENTS

10	129	4.6	2534	16	AAO95297	Plasmodium f58 contig
11	129	4.6	2534	17	AAAT16303	hFas coding sequen
12	129	4.6	2534	18	AAV32993	hFas cDNA. Mammali
13	127.4	4.5	2534	18	AAV07002	Human Fas antigen
14	63.6	2.2	19307	17	AAAT27558	Shuttle vector pad
15	62.6	2.2	2435	17	AAAT27557	Shuttle vector pad
16	60	2.1	35100	19	AAV68854	Human lung tumour
17	59.8	2.1	35100	22	AAV20441	Human c-fms oncoge
18	59.8	2.1	35100	22	AAV20441	DNA encoding Colon
19	59.2	2.1	35100	22	AAV20441	EP-892047 Seq ID 4
20	56.2	2.0	38886	20	AAO121710	Murine LOBO homolo
21	56.2	2.0	38886	20	AAO121710	Diclyostelium plas
22	54.8	1.9	13545	22	AAAT34572	Human nervous syst
23	54.8	1.9	13545	22	AAAT34572	Human metastasis a
24	54.4	1.9	8342	24	AAAT34500	Human immune syste
25	54.4	1.9	8342	24	AAAT34500	Human polynucleoti
26	54.2	1.9	10640	21	AAAT6417	Nucleotide sequenc
27	54	1.9	10640	21	AAAT6417	Human polynucleoti
28	53.4	1.9	4406	22	AAAT07188	Human actin 14 cod
29	53.2	1.9	2467	24	AAAT7407	Human immune syste
30	53.2	1.9	2467	24	AAAT7407	Human immune syste
31	53	1.9	21537	24	AAAT33999	Human immunoglobu
32	52.8	1.9	16033	21	AAAT33404	Human immune syste
33	52.8	1.9	162450	21	AAAT33404	Human immunoglobu
34	52.6	1.9	12138	24	AAAT70808	Human immune syste
35	52.6	1.9	15484	22	AAAT58432	Human immune syste
36	52.6	1.9	8622	22	AAAT58432	Human polynucleoti
37	52.4	1.8	8899	22	AAAT58432	Human polynucleoti
38	52.2	1.8	11960	22	AAAT58432	Human polynucleoti
39	52	1.8	11960	22	AAAT58432	Human polynucleoti
40	51.8	1.8	20813	20	AAAT77314	Human DNA marker
41	51.6	1.8	536	20	AAAT77314	Human immune syste
42	51.6	1.8	12404	22	AAAT6590	Human immune syste
43	51.6	1.8	24259	22	AAAT6590	Tumour suppressor
44	51.6	1.8	24259	22	AAAT6590	Human immune syste
45	51.6	1.8	39380	22	AAAT74027	Human immune syste

RESULT 1

AAAT34162	standard: DNA: 1608 BP.
ID	AAAT34162
XX	AAAT34162;
AC	22-OCT-1996 (first entry)
XX	Fas promoter region.
DE	Fas gene promoter; apoptosis; ageinf; autoimmune disease;
XX	Fas gene promoter; apoptosis; ageinf; autoimmune disease;
KW	T-cell senescence; ss.
OS	Homo sapiens.
XX	
PH	Key
FT	promoter
FT	Location/Qualifiers
FT	1..1074
FT	/*tag= a
FT	/note= "Fas gene promoter region"
FT	147..151
FT	/*tag= b
FT	/function= GFI transcription factor binding site
FT	/note= "Claim 7"
FT	168..174
FT	/*tag= c
FT	/function= EBP20 transcription factor binding site
FT	272..276
FT	/*tag= d
FT	/function= Myb transcription factor binding site
FT	/note= "Claim 9"
FT	349..353
FT	/*tag= e
FT	protein_bind

Query Match	31.1%	Score 879.4	DB 24	Length 1608:	Gaps 1
Best Local Similarity	77.1%	Fed. No. 2,6e-2321	Indels		
Matches 1083:	Conservative	0: Mismatches 321:			
767	agagaaagccatcatcatccctccttaccacactcttctcctatgacatacagctctactg	886			
1602	ACAAAAATACCTTATACCATTCCTCTTATCCACTCTCTTTATATCTATTAATAATCA	1543			
827	gagtgctgacaaagcggcgacggccgaaggtcttcctcctatgacatacagctctactg	946			
1542	AAATATATACCAAACTACACGCCCAAAATCTCTCTCAATACTAATCAATCTACTAA	1483			
887	aaggtggaacaagagacaagcctatcaaacctacaagactggtggaagtgcagtag	1423			
1482	AAAAATAAACAAAAACCAACCTTACACACCTACCAAACTATATATATATATATATAT	1006			
947	atgcaaaacacagagtgatggaagagccctcagagaggtacacactactagattgagggc	1363			
1422	ATACAAACACCAAAAT	1066			
1007	ccaaacaggtctcagaagaaatgtaacactgagagagagagcctgaaagtgcacagtgagc	1303			
1362	CCAAACAACTCCAAAAAAAT	1126			
1067	taagcaagaggtatattaactgcttactaactggttgcacttaacttcggagagagagag	1243			
1302	TAAACAAAAATTTAT	1186			
1127	ctgcagagtgaggtgcagagcctggtgcagagatgcagcaagaagaaactgaaactgagtg	1183			
1242	TTACAAAAATTAATACAAACTTATATATATATATATATATATATATATATATATATAT	1246			
1187	tgctcagctgcgaactgcgtccacaattcaggttcagtgatgctgcatctatccataacata	1123			
1182	TATCCAAATCTTAATACATACATCCAAATTCATTAATATATATATATATATATATATAT	1306			
1247	cctctgtgaaatcatatgctgaacactaccacaaagagctatctacagctccaaagaaatg	1063			
1122	CCTCTATATAAATCTATACCTTAACTACCTTAACTACCTTAACTACCTTAACTACCTTAA	1003			
1307	acttgaaacagtgctaccagagagacaaagaattacaagattttttttaaagaataat	1426			
1062	ACTTTAAACAAATTTACCCAAACACGAAACAAAAATTTTCAAAATTTTTTTTTTAA	943			
1367	ggcgaagaataatgtaagaaagggcgaagaagaattggaaggttaatatagctgg	1486			
1002	AACCAAAAAAT	883			
1427	ggctatcgatttggtcttaagtgttagctgttcttcctcttgagaataataaactaag	1546			
942	AACCTATACATTTAACTTAATATATATATATATATATATATATATATATATATATAT	823			
1487	gggcctcccttccagagccctatgagcgaacatctgcaacttgcatttccatagtgtacg	1606			
882	AAACCCCTCCCTTTCAAAACCTTATACGCAACATCTATACCTTTTTCATTAATATAT	763			
1547	tcacatccaggaacgtctgtgagcctcctcatgttgagagcacaacatgagacgcccgctc	1666			
822	TCCATTCAAAAAGGCTTAAACCTCTCAATATACACCACAAAAAATTAACCAACCATATC	703			
1607	aaagcccgcaagctctctctctgagtgactcagcaattgacaaagcctcctgtaacca	1726			
762	AAATACCCCGCAATCTTCTCTTAATTAATCACTCAACATTAACCAAAAACTCTATACCA	643			
1667	ggaggaactctgcgctctgagctccatctccttcaagactccccaactcccgagtt	1786			
702	AAACAAACCTCTACGCTCTAACTCAATCTCTCCCTCAAAACCTCCCAAACTTCCCAAAAT	583			
1727	gaactaagagagaagcctttagaaagggcagagagcggcgctctcgagaggtccctcacctgaa	1846			
642	AAACTACACAAAAACCTTTAAAAAAACCAAAAAACGAGCTCTGAAATCTCACTCTAA				
1787	gtgagcatgcccagccactgaggaacgcgccggagcagaatgccaattgtgcaacgaa				

1; 0 other;

[illegible]

79 aaagtgtgaacglttagggcttttcttaagatatttatgaagaagtgcgaacag 89

959 gggtgatggaagccctcagaacacctat
cccccaataattataaagtgtgtaagtgtgatcatgttaaataata 198

259 tagaagaataatgtcaactgaggaagcctgaagatgaacagtggcctaagcaagcct 258

1139 tattaatggtatttaattgaatttaattggaagcagagaggttcagagtgag 1138

1199 aactgcattccaaattcaggttcagtaatgataatcatctt
|| || | || || || || || || || || || || || ||
|| || || || || || || || || || || || || || ||

438

498
499 ttatgtaaatattttaagaattttttaaagcagtctacgttcacaagaacatagttgacttgaacagt 1318

atgaqtacgaaagcaaacctcgcggcgccggaata
| | | | |
tataagaatttttaagaacaatttgtttaaaaah

1379 1380 1381 1382 1383 1384 1385 1386 1387 1388

439 tggcttaagtcgtctagccttctgttttcctctctgagaaataaaaactctt
 679 ttt

[illegible][illegible]

cccccgcattcaggtagatctt 918

[illegible]

PF 16-JUL-1998; 98WO-US14//1.
XX

FT	mat_peptide	2
FT		

slg-peptide
FT

mat_peptide

FT conflict /product= Fas-antigen
 FT 1046 /tag= C
 FT /note= "this residue is not present in pF3"
 FT polyA_signal 1831..1836 /tag= d
 FT polyA_signal 2352..2357 /tag= e
 FT polyA_signal 2518..2523 /tag= f
 PN EP510691-A.
 XX 28-OCT-1992.
 PD 24-APR-1992; 92EP-0107060.
 XX 26-APR-1991; 91JP-0125234.
 XX (OSAB-) OSAKA BIOSCIENCE INST.
 XX Itoh N, Nagata S, Yonehara S;
 PI WPI: 1992-358914/44.
 DR P-PSDB: AAR28084.
 XX
 PT DNA encoding human cell surface antigen - used to clarify
 PT apoptosis mechanism of various types of cell, and to prepare
 PT monoclonal antibodies that react with tumour cells expressing Fas
 PS Claim 3; Fig 1 and 2; 27pp; English.
 XX
 CC A CDNA library was prepared from polyA+ RNA from the human lymphoma
 CC cell line KT-3. The cDNA was ligated to BstXI-cut vector pCEV4 via
 CC BstXI linkers. The KT3 CDNA library was used to transfect monkey COS-
 CC 7 cells which were then suspended in buffer containing murine anti-Fas
 CC Ab. The cells were "panned" on plates pre-coated with goat anti-mouse
 CC antibodies. The Fas-expressing cells adhered to the plates.
 CC Extrachromosomal DNA was prepared from adhered cells and used to
 CC transform E.coli VM100 cells. A 520bp XhoI-BamHI fragment from a
 CC positive clone (pF3) was used to screen the KT-3 CDNA library. The
 CC longest cDNA clone was designated pF58 and contains an ORF corresp.
 CC to a 335 amino acid pre-protein and a 319 amino acid mature protein
 CC (i.e. human Fas antigen).
 XX
 SQ Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match 4.6%; Score 129; DB 13; Length 2534;
 Best Local Similarity 100.0%; Pred. No. 9.2e-25;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 gacgctctggggagtgaggaagcggtttacgagtgaactgtgctgagcctcagggcg 2093
 DB 1 gacgctctggggagtgaggaagcggtttacgagtgaactgtgctgagcctcagggcg 60
 QY 2094 ggcactggcagcgaacacacctgagccagcctgtgctgccagggcgagctgcctt 2153
 DB 61 ggcactggcagcgaacacacctgagccagcctgtgctgccagggcgagctgcctt 120
 QY 2154 ctccgcgcg 2162
 DB 121 ctccgcgcg 129

RESULT 10
 AAQ95297 standard; cDNA; 2534 BP.
 AC AAQ95297;
 XX 19-FEB-1996 (first entry)
 DT
 XX

DE Plasmid pF58 contg. human Fas cDNA.
 XX
 KW Plasmid pF58; human Fas cDNA; soluble membrane protein;
 KW antibody production; diseases; treatment; prevention; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 195..1202
 FT sig_peptide 195..242
 FT mat_peptide 243..1199
 FT /tag= b
 FT /tag= c
 PN JP07115988-A.
 XX
 PD 09-MAY-1995.
 XX 26-OCT-1993; 93JP-0267644.
 XX 26-OCT-1993; 93JP-0267644.
 XX 26-OCT-1993; 93JP-0267644.
 XX (NISB) JAPAN TOBACCO INC.
 XX
 DR WPI: 1995-202847/27.
 DR P-PSDB: AAR78606.
 XX
 PT Preparation of soluble membrane proteins - for their use in antibody
 PT production for the treatment and prevention of related diseases
 PS Example 1; Pages 15-17; 51pp; Japanese.
 XX
 CC AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The
 CC plasmid was used in the construction of an expression vector for
 CC the prodn. of recombinant soluble membrane proteins. The proteins
 CC can be used in antibody prodn. for the treatment and prevention of
 CC related diseases.
 XX
 SQ Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match 4.6%; Score 129; DB 16; Length 2534;
 Best Local Similarity 100.0%; Pred. No. 9.2e-25;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 gacgctctggggagtgaggaagcggtttacgagtgaactgtgctgagcctcagggcg 2093
 DB 1 gacgctctggggagtgaggaagcggtttacgagtgaactgtgctgagcctcagggcg 60
 QY 2094 ggcactggcagcgaacacacctgagccagcctgtgctgccagggcgagctgcctt 2153
 DB 61 ggcactggcagcgaacacacctgagccagcctgtgctgccagggcgagctgcctt 120
 QY 2154 ctccgcgcg 2162
 DB 121 ctccgcgcg 129

RESULT 11
 AAT16303
 ID AAT16303 standard; cDNA; 2534 BP.
 AC AAT16303;
 XX 06-SEP-1996 (first entry)
 DT hFas coding sequence from plasmid pCEV4/hFas.
 XX
 DE Fas; antigen; immunoassay; monoclonal antibody; autoimmune disease; SLE;
 KW rheumatoid arthritis; serum; systemic lupus erythematosus; ss.
 XX
 OS Synthetic.

RESULT 14
 ID AAT27558
 AC AAT27558 standard; cDNA; 19307 BP.
 DT AAT27558;
 DE 07-AUG-1996 (first entry)
 SH Shuttle vector PADbel.CMWdys.
 KW Adenovirus type 5; Ad5; vector; gene therapy; gene transfer;
 helper virus; dystrophin; muscular dystrophy; ds; cyclic.
 OS Synthetic.
 PN M09613597-A2.
 PD 09-MAY-1996.
 PF 27-OCT-1995; 95MO-US14017.
 PR 28-OCT-1994; 94US-0331381.
 PA (TYPE-) UNIV PENNSYLVANIA.
 PI Chen S, Fisher KJ, Weltzman M, Wilson JM;
 DR WPI; 1996-251463/25.
 PT Recombinant adenovirus produced from shuttle vector and helper virus
 transgene(s) to target cells
 PS Example 9; Flg 12A-12P; 149pp; English.
 CC Shuttle vector PADbel.CMWdys (AAT27558) comprises the adenovirus
 cis elements needed for replication and virion encapsidation but
 is deleted of all viral genes. It carries a mouse dystrophin
 minigene under control of the CMV promoter. It is used with a helper
 infection that supplies the sequences needed for a productive viral
 adenovirus but which has disabled packaging function. Recombinant
 delivery to host cells and the ability to stably integrate the
 transgene into the host cell chromosome. Such a vector can be used
 to transfer the dystrophin gene for use in muscular dystrophy gene
 therapy.
 Sequence 19307 BP. AATC

Matches	93;	Conservative	65.58;	DB 17;	Length 19307;
OV	3114				

[illegible]

Mon Sep 9 09:30:40 2002

us-09-834-291-4.rng

Page 11

```
DB 16048 ccggcgccctgacgtgcccacgtacacgtacgtgacccgcgacatgtacaga 16107
DB 2174 gctcgagagtagtactagtgccagctggccgctgacaccttaagcttaaggtctgagag 2233
DB 16108 gctcgagagtagtactagtgccagctggccgctgacaccttaagcttgcacgtgcccgt 16167
DB 2234 gggcccccgttgagagagaga 2255
DB 16168 tttaacagctcgagacgtgagaa 16189

RESULT 15
AAT27557/c standard: cDNA: 9972 BP.
ID AAT27557
AC AAT27557:
XX 07-AUG-1996 (first entry)
XX Shuttle vector pAdDel.CBCFTRZ.
XX Adenovirus type 5; Ad5; vector: gene therapy; gene transfer;
XX helper virus: cystic fibrosis transmembrane conductance regulator;
XX CFTR; ds: cyclic.
XX Synthetic.
XX OS location/Qualifiers
XX FM complement (3652..3073)
XX Key repeat_unit /*tag= a INVERTED
XX /*rpt_type= adenovirus inverted terminal repeat"
XX /*note= "3, adenovirus (3887..3684)
XX /*tag= b complement (8622..4065)
XX /*tag= c complement (9241..8684)
XX /*tag= d CFTR gene
XX /*function= CFTR gene
XX /*complement (9241..8684)
XX /*tag= e CMV enhancer/beta actin promoter
XX /*function= (9611..9254)
XX /*complement (9611..9254)
XX /*tag= e INVERTED
XX /*rpt_type= adenovirus inverted terminal repeat"
XX /*note= "5, adenovirus (9374..9360)
XX /*tag= f complement (9374..9360)
XX /*function= packaging sequence PAC I
XX /*complement (9374..9360)
XX /*tag= g packaging sequence PAC II
XX /*function= (9353..9340)
XX /*complement (9353..9340)
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XX /*tag= j packaging sequence PAC V
XX /*function= packaging sequence PAC V

W09613597-A2.
XX 09-MAY-1996.
XX 27-OCT-1995; 95WO-US14017.
XX 28-OCT-1994; 94US-0331381.
XX (UYBE-) UNIV PENNSYLVANIA.
XX Chen S, Fisher KJ, Weltzman M, Wilson JM.
XX WPI; 1996-251463/25.
```

```
XX Recombinant adenovirus produced from shuttle vector and helper virus
XX - has crippled packaging function, useful for delivering
XX transgene(s) to target cells
XX
XX Example 4; Fig 7A-7H; 149pp; English.
XX
XX Shuttle vector pAdDel.CBCFTR (AAT27557) comprises the adenovirus
XX cis elements needed for replication and virion encapsidation but
XX is deleted of all viral genes. It carries a CFTR gene under
XX the control of a chimeric CMV enhancer/chicken beta-actin promoter.
XX It is used with a helper virus that supplies the sequences needed for
XX a productive viral infection but which has disabled packaging function.
XX Recombinant adenovirus is produced that is characterized by high titer
XX transgene delivery to host cells and the ability to stably integrate the
XX transgene into the host cell chromosome. Such a vector can be used
XX to transfer the CFTR gene for use in cystic fibrosis gene therapy.
XX
XX Sequence 9972 BP; 2581 A; 2362 C; 2245 G; 2784 T; 0 other:
XX
XX Query Match 2.2%; Score 62.6; DB 17; Length 9972;
XX Best Local Similarity 65.2%; Pred. No. 4.8e-06; Mismatches 49; Gaps 0;
XX Matches 92; Conservative
XX
XX DB 2115 ctgagcgccgcccgtgctgcccagcgagcgagcctctctcccgcgagacatgtacaga 2174
XX 2980 CGGCCGCTGCGAGCTGCGCCGATACGCTGCGGACCGGCGGACATGTACAGAG 2921
XX QY 2175 ctgagagagtagtactagtgccagctggccgctgacaccttaagcttaaggtctgagag 2234
XX DB 2920 CTCGAGAGTACTAGTGTGCGCCACGTGGCGGTGACACTTAAGCTTGACCTGCGCGCTT 2861
XX QY 2235 gggcccccgttgagagagaga 2255
XX DB 2860 TTACACAGCTGCTGACTGCGAA 2840

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Mon Sep 9 09:30:42 2002

us-09-834-291-4.inpm

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
September 7, 2002, 22:33:42 ; Search time 13836.9 Seconds
(without alignments) updates/sec
4420.187 Million cell

US-09-834-291-4
2827
1 tggagacttcacgaatg.....tgactatcaagaagacgctg 2827
Perfect score:
Sequence:
Scoring table:
Gapop 10.0, Gapext 1.0
21979536 seqs, 10817449327 residues
43959072

Searched:
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3	2370.6	83.8	45121	36	US-09-834-722-10
4	2346.6	83.0	2165	32	US-09-834-722-11
5	1714.4	60.6	2165	32	US-09-834-722-12
6	1714.4	60.6	2165	32	US-09-834-722-13
7	1372.8	48.6	1608	7	US-08-377-522C-1
8	1372.8	48.6	1608	7	US-08-377-522C-2
9	1372.8	48.6	1608	7	US-08-377-522C-3
10	706	25.0	3814	71	US-09-834-291-2
11	611.8	21.6	720	32	US-09-834-291-1
12	424.2	15.0	449	18	US-09-834-291-1
13	424.2	15.0	449	18	US-09-834-291-1
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15	424.2	15.0	449	18	US-09-834-291-1
16	424.2	15.0	449	18	US-09-834-291-1
17	424.2	15.0	449	18	US-09-834-291-1
18	424.2	15.0	449	18	US-09-834-291-1
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20	424.2	15.0	449	18	US-09-834-291-1
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24	424.2	15.0	449	18	US-09-834-291-1
25	424.2	15.0	449	18	US-09-834-291-1
26	424.2	15.0	449	18	US-09-834-291-1
27	424.2	15.0	449	18	US-09-834-291-1
28	424.2	15.0	449	18	US-09-834-291-1
29	424.2	15.0	449	18	US-09-834-291-1
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35	424.2	15.0	449	18	US-09-834-291-1
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40	424.2	15.0	449	18	US-09-834-291-1
41	424.2	15.0	449	18	US-09-834-291-1
42	424.2	15.0	449	18	US-09-834-291-1
43	424.2	15.0	449	18	US-09-834-291-1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution.
and is derived by analysis of the total score distribution.

SUMMARIES

32 190.2 6.7 466 17 US-09-333-909-2214
 33 190.2 6.7 466 31 US-09-817-500-2214
 34 188.4 6.7 532 29 US-09-726-788-5938
 35 188 6.5 565 25 US-09-552-124-2645
 36 182.6 6.5 473 16 US-09-334-611-3879
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ALIGNMENTS

Sequence 2214, Ap
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RESULT 1
 US-09-834-291-4
 Sequence 4, Application US/09834291
 GENERAL INFORMATION:
 APPLICANT: Kramer, Peter
 APPLICANT: Muller-Schilling, Martina
 TITLE OF INVENTION: P53 Binding Areas
 FILE REFERENCE: 4121-122
 CURRENT APPLICATION NUMBER: US/09/834,291
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: PCT/DE99/03343
 PRIOR FILING DATE: 1999-10-18
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 2827
 TYPE: DNA
 ORGANISM: Homo Sapiens
 US-09-834-291-4

Query Match
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Page 5

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Mon Sep 9 09:30:42 2002

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Page 7

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RESULT 7
 US-08-377-522-1
 Sequence 1, Application US/08377522
 GENERAL INFORMATION:
 APPLICANT: Mountz, John D.
 APPLICANT: Liu, Changdan
 APPLICANT: Cheng, Jianhua
 APPLICANT: Koopman, William J.
 TITLE OF INVENTION: Human Fas Gene Promoter Region
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: US
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/377, 522
 FILING DATE: 20-Jan-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

NAME: Serlich, Gary J.
 REGISTRATION NUMBER: 34,430
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1608 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
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 US-08-377-522-1

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 Db 547 ACTTGAACAGTGTTCACACAGAGCAGCAAGAAATTAACAAGTTTGTAAAGAAATTT 606
 QY 1367 ggcgaagaataatgatacgaagaagcagcagcagcagcagcagcagcagcagcagcagc 1426
 Db 607 GGCAGGAATAATGATGATAACGAAGACAGAGATTAATGTAATGTAATGTAATGTAATGTA 666
 QY 1427 ggcatacgattgtgataatgt 1486
 Db 667 GGCATGCGATTGTGCTTAAGTTGT 1486
 QY 1487 ggcgcctccttccagagcctatgagcagaacatcgtacttcttcatatgtgttaactg 1546

Query Match	48.6%	Score 1372.8	DB 7	Length 1608
Best Local Similarity	99.4%	Pred. No. 2,4e-287	Indels 7	Gaps 1
Matches 1388	Conservative	0	Mismatches	
<p>ATTORNEY/AGENT INFORMATION: NAME: Benjamin Aaron Adler, Ph.D., J.D. REGISTRATION NUMBER: 35,423 REFERENCE/DOCKET NUMBER: D5919 TELECOMMUNICATION INFORMATION: TELEPHONE: (713) 777-6908 TELEFAX: (713) 777-2321 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1608 bp TYPE: nucleic acid STRANDEDNESS: double-stranded TOPOLOGY: linear MOLECULE TYPE: genomic DNA DESCRIPTION: no HYPOTHETICAL: no ANTI-SENSE: no FRAGMENT TYPE: ORIGINAL SOURCE: ORGANISM: human TISSUE TYPE: placental IMMEDIATE SOURCE: LIBRARY: (FIX1; EMBL-SP6/17 CLONE: FIX1, FIX3, EMBL1, EMBL2, EMBL3 POSITION IN GENOME: FEATURE: PUBLICATION INFORMATION: US-08-377-522C-1</p>				
QY	767	agagaatgccatatacactccctactccactcttlltggctattatagatgctca	826	
DB	7	ACAGAGATCCCTCTATACATCTCTCTATCCACTCTTTTGGTCAATAGATGCTCA	66	
QY	827	gagtgtgtcacaaagcttggcaagccaggggtcttcctcatatgcaactacagctactga	886	
DB	67	GAGTGTGTGCACAAGGCTGGCAGCCAGGGTCTTCCTCATATGGCACTTAACACTTACGTA	126	
QY	887	aaggtggaacagagagcaagcctactcaacactcaagaagctgtgttaagtgcagtgacag	946	
DB	127	AAGGTGGAACAGAGACACAGCCTATCAACACTTCAAGACTGGGGTAAGTGCAGTGACAG	186	
QY	947	atgcaaaacacagagggtgtagaaagccctcagagaggttaacctaaactaactgaatttgaagc	1006	
DB	187	ATGCAAAACACAGAGGTGTGTGAAGCCCTCAGAGGGGTAACTTAACCTAGATTGAGGCC	246	
QY	1007	ccaaacaggtcccaagaagaatgtlcaacttgaagagagaagccttgaagagatgaacagttggc	1066	
DB	247	CCAAACAGGCTCCAGAAAGAAATGTCAACTGAGAGGAGCCTGGAAGATGAACAGTGGGC	306	
QY	1067	taagcaaaaggttattatgtgtgttattatgtgttgaatctaatgtgggaagggagagag	1126	
DB	307	TAAAGCAAAAGGTTATTAAATGTGTTATTATGGGTTGAATCTTAATGGGAGAGGAGACAGG	366	
QY	1127	ttcgaagtagagtgacagagcttgtgtgacagatgccaaagagaatactgaacactttagtg	1186	
DB	367	TTGCAAGTAGAGTGACAGACTTGTGGAGCAGGACCCAAAGAAATCTGAAACTTTAGTG	426	
QY	1187	tgctcagtcgtgaactgcatcccaaatccaaatccaggttcagtaatgtagtcatatccaaacata	1246	
DB	427	TGTCAGACTGGAAGTGTGATGCTCAAAATTCAGAGTCAAGTCAATTAATCCAAACATA	486	
QY	1247	ccttcgttaaatctcatgcttaactactactaagagctatccacglltccaaagcaatagtg	1306	
DB	487	CTTCTGTGAATAATTCATCTTAACCTTAACCTTAAGAGCTTATCAGCTTCCAAAGCAATAGTG	546	
QY	1307	actttggaacaggttcacacagagcagaaagaatatacagaatttllttaaagaanaatt	1366	
DB	547	ACTTTGAACAGTGTTCACCAAGACAGAAAGAAATTAACAAGATTTTTTTAAAGAAATAT	606	

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1187 tgcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1246
1247 tctccagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 486
1247 tctccagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1306
1247 tctccagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 546
487 ccttcgtaaaatcgaatcgaatcccaatcaggttgaatgatcattatccacaata 1366
1307 acttgaacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 606
547 acttgaacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1426
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607 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1486
1427 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 726
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1487 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 786
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787 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1666
1607 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 906
847 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1726
1667 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 966
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1727 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1026
967 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1846
1787 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1085
1027 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1906
1847 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1145
1086 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1966
1907 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1205
1146 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 2026
1967 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1265
1206 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 2086
2027 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1325
1266 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 2146
2087 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1385
1326 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1385
2147 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 2162
1386 ggcacagtcggaatcgaatcccaatcaggttgaatgatcattatccacaata 1401

APPLICANT: Morris, MacDonald
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
FILE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEO ID NO: 29531
LENGTH: 3814
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 415714.1
US-60-324-185-29531
Query Match 25.0%; Score 706; DB 71; Length 3814;
Best Local Similarity 99.9%; Pred. No. 2.3e-142;
Matches 717; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1446 agttgtaagcttggcttctctctgagaataaaactaaggagccctcttcaag 1505
DB 1 agttgtaagcttggcttctctctgagaataaaactaaggagccctcttcaag 60
QY 1506 cccatgagcgaacacatcgtacttttcatatggttaacttccattccaggaagctg 120
DB 61 cccatgagcgaacacatcgtacttttcatatggttaacttccattccaggaagctg 1625
QY 1566 tgaagctcctatggttcagccacacatgagacagccagtcgaatgcccgaagctt 180
DB 121 tgaagctcctatggttcagccacacatgagacagccagtcgaatgcccgaagctt 1685
QY 1626 ctctgagtgactcagcaattgagcagctctctgacacagcagagcttgcct 240
DB 181 ctctgagtgactcagcaattgagcagctctctgacacagcagagcttgcct 1745
QY 1686 gactcattctctcctcgaagcctcccaactcccaagttgacacagcagaagctt 300
DB 241 gactcattctctcctcgaagcctcccaactcccaagttgacacagcagaagctt 1805
QY 1746 tagaaggcagagagcagcagctcctgagctcctcagctgaagtgaagcagcagct 360
DB 301 tagaaggcagagagcagcagctcctgagctcctcagctgaagtgaagcagcagct 1865
QY 1806 caggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
DB 361 caggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1925
QY 1866 ctgacttctccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 480
DB 421 ctgacttctccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1985
QY 1926 ccaaccgagcgttcccaagcagcagcagcagcagcagcagcagcagcagcagcagc 540
DB 481 ccaaccgagcgttcccaagcagcagcagcagcagcagcagcagcagcagcagcagc 2045
QY 1986 gtagcctcgtctctgactcctcgaagagtgacacagcagcagcagcagcagcagcagc 600
DB 541 gtagcctcgtctctgactcctcgaagagtgacacagcagcagcagcagcagcagcagc 2104
QY 2046 gtagcaggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660
DB 601 gtagcaggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2162
QY 2105 ggaacacacccctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 718
DB 661 ggaacacacccctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc

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RESULT 12
US-09-404-284-674/c
; Sequence 674, Application US/09404284
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 20411-780
; CURRENT APPLICATION NUMBER: US/09/404,284
; NUMBER OF SEQ ID NOS: 4670
; SOFTWARE: Hy-Patent.pl Version 3.1
; SEQ ID NO 674
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-404-284-674

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Query Match      15.0%; Score 424.2; DB 18; Length 449;
Best Local Similarity 99.3%; Pred. No. 1.7e-81;
Matches 426; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

QY 1680 gcctcgaagtcctatctctcctcccaagacctccccaacttcccaaggtltaaacatagcaga 1739
Db 449 GCTTCTGAGCTCCATTTCTCTTCAAGACCTCCCAACTTCCAGGTTGMACTACAGCAGA 1739
QY 1740 agcccttagaagagcagagagcgagctctcgaagtlctcaccgtgaagtatgcatgcag 1799
Db 389 AGCCTTTAGAAAGGACAGAGAGGCGGCTCTGAGGTCTCTACCTGAAATGAGCATATGCCAG 1799
QY 1800 ccactcagaagacgcccccgagacagaaatgccaattgttgaacgaaccctgactcctc 1859
Db 329 CCACTGACAGAGACGCCCGGAGACAGAAATGCCATTGTGTCAACGAACCCGACTCTTC 1859
QY 1860 ctacaccttgactctccctccctccctaccgcgcgcaagcgaaagttgctgaatcaatggag 1919
Db 269 CTCACCTGACTCTCTCCCTCCCTCCCTACCCGCGGACGGCCAAATTGCTGAAATCAATGGAG 1919
QY 1920 ccctccccaaccgcggcgttccccaagcagagctcctccatccctctcgaaccacgcggag 1979
Db 209 CCGTCCCCCAACCCGGGCGTTCGCCACGAGGCTCTCTTCCATCTCCYCGACCAACCGGGG 1979
QY 1980 ctttcgtgaagctctctctgaatctcgcgcaagatgacacacagtggttcaaaagacct 2039
Db 149 CTTTTCGTGAGCTGCTCTCTGATATCGGGCAAGAGTGAACACAGGTGTCAAAAGACCT 2039
QY 2040 tcttgaggagttaaggaaacgggtttacagagtactgctctgaagctcgaagcgagggacct 2099
Db 89 TCTGGGGAGTGAGAAAGCGGTTTACGAGTACTGTGGCTGAGGCTCAGGGCGGCACT 2099
QY 2100 ggcacgcaa 2108
Db 29 GGACACGGGA 21

RESULT 13
US-09-524-038-674/c
; Sequence 674, Application US/09524038
; GENERAL INFORMATION:
; APPLICANT: Dermanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark C.
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 780CIP
; CURRENT APPLICATION NUMBER: US/09/524,038
; EARLIER FILING DATE: 2000-03-13
; EARLIER APPLICATION NUMBER: 09/404,284
; EARLIER FILING DATE: 1999-09-21

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NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 674
LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
US-09-524-038-674

Query Match 15.08; Score 424.2; DB 19; Length 449;
Best Local Similarity 99.3%; Pred. No. 1.7e-81;
Matches 426; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1680 cgccttgagctccatctccctcaagacctcccaactcccaagltgaatacagcaga 1739
DB 449 CGTCTGAGCTCATTCTCTTCAAGACCTCCCAACTCCAGGTTGAATACAGACAGA 390
QY 1740 agccttgaagaagcagcagcagcagcagcagcagcagcagcagcagcagcag 1799
DB 389 AGCCTTGAAGAAGGCGCAGAGCGCGCTCTCGAGTCTCAGCTGAGTGAAGCAGCAG 330
QY 1800 ccactgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1859
DB 329 CCACCTGAGAGAGCGCGCGGACAGGAATGCCATTGTGCAAGCAAGCCTGACTCTTC 270
QY 1860 ctcaacctgactctccctccctccctccctccctccctccctccctccctccctcc 1919
DB 269 CTCACCCCTGACTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 210
QY 1920 cccctcccaaccccgagcagcagcagcagcagcagcagcagcagcagcagcagcag 1979
DB 209 CCTCCCAACCCGCGCGCTCTCCCAAGAGCTCTCTCCCAATCTCTCCCAAGCGGG 150
QY 1980 cttcttgagctcgcct 2039
DB 149 CTTTGTGAGCTCGTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 90
QY 2040 tctggagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2099
DB 89 TCTGGGAGTGAAGAGAGCGGTTTACAGTACTTGGCTGAGGCGGCGGACT 30
QY 2100 ggcacggaa 2108
DB 29 GGCACGGGA 21

RESULT 14

US-09-306-350A-14682/c
Sequence 14682, Application US/09306350A
GENERAL INFORMATION:
APPLICANT: Dickson, Mark C.
APPLICANT: Drmanac, Radoje T.
APPLICANT: Jones, Lee W.
APPLICANT: Labat, Ivan
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 20411-776
CURRENT FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
SOFTWARE: pt_CT_1 Version 1.1
SEQ ID NO 14682
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-350A-14682

Query Match 11.3%; Score 319.6; DB 17; Length 458;
Best Local Similarity 96.3%; Pred. No. 9.1e-59;
Matches 391; Conservative 0; Mismatches 9; Indels 6; Gaps 6;

QY 961 gtgatgaaagccctcaagaggtgaactaactagatttgaggcccaagctcca 1020
DB 457 GTGATGAAAGCCCTCAGAGGAGGTAACTAAGTATTTGA-GGCCCAAGAGGCTCCA 399
QY 1021 gaagaanaatgcaactgaggaagcctgaagatgaacagtggtgagcaagaggtta 1080
DB 398 GAAGAAATGTCAACTGAG 340
QY 1081 ttaatgttttaattggttgatgaactaattggaagaggaagaggttgdaagtaggt 1140
DB 339 TTAATGTGTTAATGAGGTTTAATCTAATTTGGAAGGAGAGA-GTTGCAAGATGAGGT 281
QY 1141 gaagagctgtgtgacgagatgcagaaagaactgaacattagtggttcagcttgaa 1200
DB 280 GCAGAGCTGTGTGGGAGAGCCAAAGAAATTAAGAACTTTAG-GTGTCCAGTCTGAA 222
QY 1201 ctgacatcaaatcagtggtcagtaataatgagtaataatcaacataactctgttaa 1260
DB 221 CTGACATCAAAATTCAGGTTCAAGTATGATGATGATGATGATGATGATGATGATGAT 163
QY 1261 catgctaaactaactaagagctatctacggttccaaagcaatagtgacttgagaggt 1320
DB 162 CAGCTAACTAGTAAGAGCTATCTACGTTCCAAAGCAATAG-GACTTTGAACAGTGT 104
QY 1321 tcaacagagcagaaagaattacaagatttttttaagaagaatt 1366
DB 103 TCACCAAGAGCAGAAAGAAATTAAGATTTTTCCTGCTCCGATT 58

RESULT 15

US-09-909-629-14682/c
Sequence 14682, Application US/09909629
GENERAL INFORMATION:
APPLICANT: Dickson, Mark C.
APPLICANT: Drmanac, Radoje T.
APPLICANT: Jones, Lee W.
APPLICANT: Labat, Ivan
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 20411-776
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/306,350
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
SOFTWARE: pt_CT_1 Version 1.1
SEQ ID NO 14682
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
US-09-909-629-14682

Query Match 11.3%; Score 319.6; DB 34; Length 458;
Best Local Similarity 96.3%; Pred. No. 9.1e-59;
Matches 391; Conservative 0; Mismatches 9; Indels 6; Gaps 6;

QY 961 gtgatgaaagccctcaagaggtgaactaactagatttgaggcccaagctcca 1020
DB 457 GTGATGAAAGCCCTCAGAGGAGGTAACTAAGTATTTGA-GGCCCAAGAGGCTCCA 399
QY 1021 gaagaanaatgcaactgaggaagcctgaagatgaacagtggtgagcaagaggtta 1080
DB 398 GAAGAAATGTCAACTGAG 340
QY 1081 ttaatgttttaattggttgatgaactaattggaagaggaagaggttgdaagtaggt 1140
DB 339 TTAATGTGTTAATGAGGTTTAATCTAATTTGGAAGGAGAGA-GTTGCAAGATGAGGT 281
QY 1141 gcaagagctgtgtgacgagatgcagaaagaactgaacattagtggttcagcttgaa 1200
DB 280 GCAGAGCTGTGTGGGAGAGCCAAAGAAATTAAGATTTTTCCTGCTCCGATT 222

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QY 1201 ctgcattccaaatcagggttcagtaatgataatcattatccaaacataccttctgtaaat 1260
Db 221 CTGCATCCAAATTCAGGTTCAGTAATGATGATATTCCTCAACA-ACCTTCTGTAAAT 163
QY 1261 caagctaaactacctaagaagctatcaccgttccaaagcaatagtgactttgaacagtg 1320
Db 162 CATGCTAAACTACGTAAAGAGCTATCTACCGTTCCTCAAGCAATAG-GACTTTGAACAGTGT 104
QY 1321 tcaccagagcagcaagaattacaagaatttttttaagaagaatt 1366
Db 103 TCACCAAGAGCAGCAAGAAATTTACAGATTTTTTCTGTCGCCGAT 58

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Search completed: September 7, 2002, 22:35:39
 Job time: 44033 sec

Db 8294 gaactgagagataattgacgtacgtggtgagaggtgaggggaggggtagtgcataga 8353
OY 361 aagagcgagacgttggaggaagaata tctaaagttaattccctgacctgctattatta 420
Db 8354 aagagcgagacgttggaggaagaata tctaaagttaattccctgacctgctattatta 8413
OY 421 actaacacatcttgcgaatgttgctaaagcttttttggctacatgtttttatttgaag 480
Db 8414 actaacacatcttgcgaatgttgctaaagcttttttggctacatgtttttatttgaag 8473
OY 481 taagttaataatcactcactcactcactcactcactcactcactcactcactcactc 540
Db 8474 taagttaataatcactcactcactcactcactcactcactcactcactcactcactc 8533
OY 541 cacatatgtgagttgtggtctataatcaactcagaagatactgatttgcattgt 600
Db 8534 cacatatgtgagttgtggtctataatcaactcagaagatactgatttgcattgt 8593
OY 601 ccttccctcttcttctcctcctcctcctcctcctcctcctcctcctcctcctc 660
Db 8594 ccttccctcttcttctcctcctcctcctcctcctcctcctcctcctcctcctc 8653
OY 661 ctccctcacaaccccttctcctcctcctcctcctcctcctcctcctcctcctcctc 720
Db 8654 ctccctcacaaccccttctcctcctcctcctcctcctcctcctcctcctcctcctc 8713
OY 721 atttggaaatgatttgaatttcaaaaatttcagagataatcagaagatggccata 780
Db 8714 atttggaaatgatttgaatttcaaaaatttcagagataatcagaagatggccata 8773
OY 781 taacatctcctcctcactcactccttcttctgctcattagatgctcagatgtgtgcaca 840
Db 8774 taacatctcctcactcactccttcttctgctcattagatgctcagatgtgtgcaca 8833
OY 841 ggtctgagacgccaagggtcttccctcactcactcactcactcactcactcactcactc 900
Db 8834 ggtctgagacgccaagggtcttccctcactcactcactcactcactcactcactcactc 8893
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Db 8894 acaagcctcactcacaacactcagaagctgtgtgagtgacgtgacagatgcacaaacag 8953
OY 961 gttgtgaaagccctcagaaggtttaaactaacttgaagggcccaacaggtctc 1020
Db 8954 gttgtgaaagccctcagaaggtttaaactaacttgaagggcccaacaggtctc 9013
OY 1021 gaaagaatgtcactcactcactcactcactcactcactcactcactcactcactc 1080
Db 9014 gaaagaatgtcactcactcactcactcactcactcactcactcactcactcactc 1081
OY 1081 ttaatgtttaaattgagttgaaatcactcactcactcactcactcactcactcactc 1140
Db 9074 ttaatgtttaaattgagttgaaatcactcactcactcactcactcactcactcactc 9133
OY 1141 gcagagcttggtagcagatgcacaaaggaatactgaaccccttgaagtcagtcggaa 1200
Db 9134 gcagagcttggtagcagatgcacaaaggaatactgaaccccttgaagtcagtcggaa 9193
OY 1201 ctgcatccaatcaggttcaagtaatgtatcattatccaacataccttcttgaataat 1260
Db 9194 ctgcatccaatcaggttcaagtaatgtatcattatccaacataccttcttgaataat 9233
OY 1261 catgtctaaactcactcactcactcactcactcactcactcactcactcactcactc 1320
Db 9254 catgtctaaactcactcactcactcactcactcactcactcactcactcactcactc 9313
OY 1321 tcaacgagagcagaagaatactacaagattttttttaaagaatactgacaggaataat 1380
Db 9314 tcaacgagagcagaagaatactacaagattttttttaaagaatactgacaggaataat 9373
OY 1381 gagtaacgagagcagaagaatactgaaatgttataatagctgaggtcgtatcgattg 1440
Db 1440 gagtaacgagagcagaagaatactgaaatgttataatagctgaggtcgtatcgattg 1440

Db 9374 gagaacgaagagacaggaagtaattgtgaatgtttaatatatgctggggtcgtcgattg 9433
OY 1441 gcttaagtgttaacttgttttctcctccttgaagaataaataaaggccctcctt 1500
Db 9434 gcttaagtgttaacttgttttctcctccttgaagaataaataaaggccctcctt 9493
OY 1501 cagaagcctatgycgcaacatctgtaacttttcaatgattgattcattcagaagac 1560
Db 9494 cagaagcctatgycgcaacatctgtaacttttcaatgattgattcattcagaagac 9553
OY 1561 gtcgtgagctcactcactcactcactcactcactcactcactcactcactcactc 1620
Db 9554 gtcgtgagctcactcactcactcactcactcactcactcactcactcactcactc 9613
OY 1621 tcttctcgtgagtgactcagaacattagccaaggtcctcgttaccacggcagacccctg 1680
Db 9614 tcttctcgtgagtgactcagaacattagccaaggtcctcgttaccacggcagacccctg 9673
OY 1681 gctcgtgagctcactcactcactcactcactcactcactcactcactcactcactc 1740
Db 9674 gctcgtgagctcactcactcactcactcactcactcactcactcactcactcactc 9733
OY 1741 gctctagaagaagggagagagcggtcctcgaaggtccctcactcactcactcactc 1800
Db 9734 gctctagaagaagggagagagcggtcctcgaaggtccctcactcactcactcactc 9793
OY 1801 cactcagaagaagggcgagaggaatgccaattgtgcaacgaaacactgactcctcc 1860
Db 9794 cactcagaagaagggcgagaggaatgccaattgtgcaacgaaacactgactcctcc 9853
OY 1861 tcaacctgacttcccccctcactcactcactcactcactcactcactcactcactc 1920
Db 9854 tcaacctgacttcccccctcactcactcactcactcactcactcactcactcactc 9913
OY 1921 cctccccaacccggcggttcccccagcgaggtcttccctcactcactcactcactc 1980
Db 9914 cctccccaacccggcggttcccccagcgaggtcttccctcactcactcactcactc 9973
OY 1981 tttctgtgagctgctcctcactcactcactcactcactcactcactcactcactc 2040
Db 9974 tttctgtgagctgctcctcactcactcactcactcactcactcactcactcactc 10033
OY 2041 ctgggagtgagggaggggtttagagtgactgctcgtgagcctcagaagggcgagctg 2100
Db 10034 ctgggagtgagggaggggtttagagtgactgctcgtgagcctcagaagggcgagctg 10093
OY 2101 gaaaggaacacacccctgagggcagccctgctgctgccaagcgaggtcgtcctccgc 2160
Db 10094 gaaaggaacacacccctgagggcagccctgctgctgccaagcgaggtcgtcctccgc 10153
OY 2161 g-----gacatgtacagagctcgaagtaact----- 2187
Db 10154 ggggttgtagaccgctcagtgaggttgaggagctcttccactcagagattgctc 10213
OY 2188 ----- 2187
Db 10214 aacaacatgctggtcactcactcactcactcactcactcactcactcactcactc 2187
OY 2188 ----- 2187
Db 10274 gaggcttaaccgctcttctgctccgggagatagcaaaatgcyggcgagcgagcgtgc 10333
OY 2210 ----- 2209
Db 10334 gggatgcyggcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 10393
OY 2210 ----- 2209
Db 10394 gttgagagactggtcccgggggtgtaggacttccctcagcgccgggtgctcagagc 2209
OY 2210 ----- 2209
Db 10454 ctggagagactgcttcttctggtcctgagtgagagtgctgactccgctgaggcgagc 10513

PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9394
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. X63717
PCT-US02-25766-9394

Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-23;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2008 gcaagagtgacacacaggtgttcaagaagcgttctgggaggtgaggaagcggtttacga 2067
1 gcaagagtgacacacaggtgttcaagaagcgttctgggaggtgaggaagcggtttacga 60
QY 2068 gtgactgtgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 2127
1 gtgactgtgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 120
Db 61 ttgacttgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 120
QY 2128 ttgctgcccaaggcgagcgtctctcttcccgcg 2162
1 ttgctgcccaaggcgagcgtctctcttcccgcg 155
Db 121 ttgctgcccaaggcgagcgtctctcttcccgcg 155

RESULT 7
US-10-035-832-1263
Sequence 1263, Application US/10035832
GENERAL INFORMATION:
APPLICANT: Engelhard, Eric
APPLICANT: Morris, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
PRIOR FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1263
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
US-10-035-832-1263

Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-23;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2008 gcaagagtgacacacaggtgttcaagaagcgttctgggaggtgaggaagcggtttacga 2067
1 gcaagagtgacacacaggtgttcaagaagcgttctgggaggtgaggaagcggtttacga 60
QY 2068 gtgactgtgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 2127
1 gtgactgtgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 120
Db 61 gtgactgtgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 120
QY 2128 ttgctgcccaaggcgagcgtctctcttcccgcg 2162
1 ttgctgcccaaggcgagcgtctctcttcccgcg 155
Db 121 ttgctgcccaaggcgagcgtctctcttcccgcg 155

RESULT 8
US-10-007-926A-143
Sequence 143, Application US/10007926A

GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOULGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 143
LENGTH: 2551
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: tumor necrosis factor receptor superfamily,
US-10-007-926A-143

Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-23;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2008 gcaagagtgacacacaggtgttcaagaagcgttctgggaggtgaggaagcggtttacga 2067
1 gcaagagtgacacacaggtgttcaagaagcgttctgggaggtgaggaagcggtttacga 60
QY 2068 gtgactgtgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 2127
1 gtgactgtgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 120
Db 61 gtgactgtgctggagccctcagggcgcgagcactgagcaggaacacacccctgaagcgagccc 120
QY 2128 ttgctgcccaaggcgagcgtctctcttcccgcg 2162
1 ttgctgcccaaggcgagcgtctctcttcccgcg 155
Db 121 ttgctgcccaaggcgagcgtctctcttcccgcg 155

RESULT 9
US-09-053-375B-233
Sequence 233, Application US/09053375B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: Nucleic Acid Arrays
FILE REFERENCE: CION-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 233
LENGTH: 2334
TYPE: DNA
ORGANISM: Homo sapiens
US-09-053-375B-233

Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 gacgttcttgaggagtgagggaagcggtttacgaagtgacttgctgagcctcagggcg 2093
1 gacgttcttgaggagtgagggaagcggtttacgaagtgacttgctgagcctcagggcg 60
Db 1 gacgttcttgaggagtgagggaagcggtttacgaagtgacttgctgagcctcagggcg 60
QY 2094 ggcacttgacacggaacacacccctgagccagcccttgctgcccagcgagcgtctctt 2153
1 ggcacttgacacggaacacacccctgagccagcccttgctgcccagcgagcgtctctt 120
Db 61 ggcacttgacacggaacacacccctgagccagcccttgctgcccagcgagcgtctctt 120

QY 2154 ctccgcgcg 2162
Db 121 ctccgcgcg 129

RESULT 10

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US-10-035-832-1259
; Sequence 1259, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1259
; LENGTH: 55996
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (29253)..(29272)
; OTHER INFORMATION: "n" at positions 29253 thru 29272 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (31023)..(31239)
; OTHER INFORMATION: "n" at positions 31023 thru 31239 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (42691)..(42710)
; OTHER INFORMATION: "n" at positions 42691 thru 42710 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (46987)..(47006)
; OTHER INFORMATION: "n" at positions 46987 thru 47006 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (48271)..(48290)
; OTHER INFORMATION: "n" at positions 48271 thru 48290 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (50692)..(50711)
; OTHER INFORMATION: "n" at positions 50692 thru 50711 can be any base
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (53136)..(53155)
; OTHER INFORMATION: "n" at positions 53136 thru 53155 can be any base
; NAME/KEY: misc-feature
; LOCATION: (55549)..(55568)
; OTHER INFORMATION: "n" at positions 55549 thru 55568 can be any base
US-10-035-832-1259
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Query Match 2.4%; Score 68.2; DB 6; Length 55996;
Best Local Similarity 63.6%; Pred. No. 0.00028;
Matches 152; Conservative 0; Mismatches 83; Indels 4; Gaps 3;

QY 1272 acctaaagctatctacgttccaaagcaatgacttgaacagtggttaccac--gag 1329
Db 7739 actaaagtgtcactactttccaaacaaagtgacttgaacagtggttaccac--gag 1329
QY 1330 cagcaagaattcaagatttttttaagaagaattggtccaggaataatgagtaacga 1389
Db 7799 cagtaagaagataagaatttttttaacgaagaattgttcaggaataatccgtaacaa 7858

QY 1390 aggaacagaagtaattgtgaattttaaataagctgggcatgagattggttaagt 1449
Db 7859 aag-gaagaagtaataatgtct-aacacagcaggtgaggtttcccttaccgaat 7916
QY 1450 gtagctgttcccttgggaataaataacaaagggccctcccttccagaagcc 1508
Db 7917 agacttctcttttgaagattatattccctgcatgctcccttacccttccacc 7975

RESULT 11

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US-10-027-632-145670/c
; Sequence 145670, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145670
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-145670
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Query Match 2.2%; Score 60.8; DB 7; Length 816;
Best Local Similarity 69.2%; Pred. No. 0.0033;
Matches 83; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 697 ttttttatttaagacttcttcatcttggatagttttagatttccaaaattgca 756
Db 307 tctttttgttttaatttaatttttgccttttagaacatttttagcttgcagattattgca 248
QY 757 gagataacagaggaatgccatataccatccctccatcccttcttcttcttctat 816
Db 247 aagatagttacagaaatttccacatctgcacacccgtttccctgttttaacattttat 188

RESULT 12

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US-10-113-872-796/c
; Sequence 796, Application US/10113872
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: Fanger, Gary R.
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121,478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
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us-09-834-291-4.rtf

Page 8

Search completed: September 8, 2002, 01:14:46
Job time: 37364 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: September 7, 2002, 14:51:47; Search time 8462.63 Seconds
(without alignments)
4508.751 Million cell updates/sec

Title: US-09-834-291-4
Perfect score: 2827
Sequence: 1 tggagactctcagaatgataatg.....tgcatacaagagacgctg 2827

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database:
- 1: em_estba:*
 - 2: em_esthm:*
 - 3: em_estin:*
 - 4: em_estnu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_gss:*
 - 13: em_gss_hum:*
 - 14: em_gss_iny:*
 - 15: em_gss_pln:*
 - 16: em_gss_vit:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	465.4	16.5	467	9	AA704610 z119h02.s
2	438.4	15.5	793	10	BI763679 603049567
3	298.4	10.5	603	9	AA058563 AA058563
4	294.4	10.4	577	9	AA056275 z153b04.s
5	286.4	10.1	442	9	AA056275 z153b03.s
6	286.4	10.1	547	9	AA011028 z634d02.s
7	285.4	10.1	447	9	AA047220 z149e11.s
8	276.4	9.8	467	9	AA057418 z159h03.s
9	270	9.6	376	10	AA020992 z655f07.s
10	259	9.2	388	10	HA8126 HA8126
11	254.4	9.0	287	9	AA018441 z655e09.s1
12	253.6	9.0	381	10	HA8544 y104f01.s1
13	197	7.0	419	10	HA85827 yq22g10.s1
14	185.2	6.6	696	9	AV715411 AV715411
15	181.8	5.7	429	9	BI838027 603083875
16	161	5.2	1339	10	AM239285 xdb38d02.y
17	145.6				BG288747 602385566

18	124.2	4.4	300	9	AI100132
19	117	4.1	932	9	AL542093
20	105.4	3.7	1052	10	BM455788
21	96	3.4	283	10	BM090262
22	85	3.0	899	9	AI540709
23	80.4	2.8	1101	12	CNS00396
24	72	2.5	506	10	BG659530
25	67	2.4	1101	12	CNS00396
26	65	2.3	286	10	BI029879
27	64.6	2.3	343	10	BI045052
28	64.6	2.3	343	10	BI045083
29	64	2.3	169	10	BG998195
30	64	2.3	205	10	BG997854
31	64	2.3	267	10	BG961378
32	63.8	2.2	306	9	AA668797
33	63.6	2.2	306	10	BI004597
34	63.6	2.2	549	9	AA521324
35	63.6	2.2	583	9	AA521406
36	63.6	2.2	280	10	BG998167
37	63.4	2.2	1101	12	CNS0182P
38	63.2	2.2	275	10	BI005814
39	63	2.2	276	10	BG015436
40	63	2.2	279	10	BG978282
41	63	2.2	287	10	BF759346
42	63	2.2	319	10	BI028532
43	63	2.2	1201	12	CNS0165X
44	63	2.2	987	12	CNS016F1
45	62.8	2.2			

ALIGNMENTS

RESULT 1
AA704610 467 bp mRNA linear EST 24-DEC-1997
z119h02.s1 Soares fetal_liver.spleen.JNF1LS.S1 Homo sapiens CDNA
LOCUS
DEFINITION
clone IMAGE:450771 3', mRNA sequence.
AA704610
AA704610.1 GI:2714528
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 467)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B.,
White, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

FEATURES
source
1. 467
/organism="Homo sapiens"
/db_xref="GDB:138712"
/db_xref="taxon:9606"
/clone="IMAGE:450771"
/clone_lib="Soares fetal_liver.spleen.JNF1LS.S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)

Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 459.
Location/Qualifiers


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sequence stop: 3/2
Location/Qualifiers
1. .442

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92 a 107 c 103 g 138 t 2 others

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/organism="Homo sapiens"
/db_xref="GDB:1277412"
/db_xref="taxon:9606"
/clone="IMAGE:360867"
/clone_lib="Soares retina N2b4HR"
sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/mode="Organ: eye; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I...oligo(dT) primer [5
TGTTCACATCGAGATGGAGCCGCCGCTTTTCTTTTCTTTTCTT 3'],
adapters (Pharmacia) was size selected, ligated to Eco RI
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Patima Bonaldo."
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Query Match	10.18;	Score 286.4;	DB 9;	Length 442
Best Local Similarity	99.08;	Pred. No. 1.1e-41;		

	Matches	298 :	Conservative	0 :	Mismatches	2 :	Indels	1 :	Gaps	1
QY	2528		gtcacacagaaaagaagaactgacctgctccttcctccgcggagatctctcttaagact-gt						2586	
Db	1		gtcacacagaaaagaagaactgacctgctccttcctccgcggagatctctcttaagactmgt						60	
QY	2587		aagtcgctgcctgagtggttcaattctgtttgttttctgcacctctctctctcttt						2646	
Db	61		aagtcgctgcctgagtggttcaattctgtttgttttctgcacctctctctctcttt						120	
QY	2647		gcacctcttaagcttgacctcccatggtgtaattctgacttgctcctgctggggttggtg						2706	
Db	121		gcccttttctaagcttgacctcccatggtgtaattctgacttgctcctgctggggttggtg						180	
QY	2707		gtactcgcttccaccgcacagaaaccggcgactatattgcccagaagaacttgacagcc						2766	
Db	181		gtactcgcttccaccgcacagaaaccggcgactatattgcccagaagaacttgacagcc						240	
QY	2767		tgcttgaagaagctccctgcgtcagaatgccaagcttcagatggtcaatacaagaagcgt						2826	
Db	241		tgcttgaagaagaactccctgcgtcagaatgccaagcttcagatggtcaatacaagaagcgt						300	
QY	2827		g						301	
Db	301		g						301	

RESULT	6
AA047220	
LOCUS	
DEFINITION	547 bp mRNA linear EST 02-FEB-1997
IMAGE1.s1	Soares retina N2b4hr Homo sapiens cDNA clone
IMAGE380300.3'	mRNA sequence.
ACCESSION	AA047220
VERSION	AA047220.1 GI:1525120
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE
1 (pases 1 to 547)
Hiller, L., Lennon, G., Becker, M. (1973) Primates; Catarrhini; Homiidae; Homo.

TITLE
 JOURNAL
 MEDLINE
 COMMENT
 97044478
 Contact: Wilson RK
 Genom. Res. 6 (9), 807-828 (1996)

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FEATURES
source
Location/Qualifiers
1..547

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"organism":"Homo sapiens"
/db_xref="GDB:128857"
/db_xref="taxon:9606"
/clone="IMAGE:380300"
/clone_lib="Scars retina N2b4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ eye; Vector: pRTT3 (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; Site_3:

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strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo.

BASE COUNT 131 a 128 c 125 g 158 t 5 others
 ORIGIN
 Query Match 10.1%; Score 286.4; DB 9; Length 547;
 Best Local Similarity 99.3%; Pred. No. 1.1e-41; Indels 1; Gaps 1;
 Matches 298; Conservative 0; Mismatches 1;

QY 2528 gtcacacagaaagaacatgcctgtctccctccgggaattctctttaagactga 2587
 1 gtcacacagaaagaacatgcctgtctccctccgggaattctctttaagactga 60
 QY 2588 agtcgctgctagtggttcaattgttttttttccctctctctctctctt 2647
 61 agtcgctgctagtggttcaattgttttttttccctctctctctctctt 120
 DB 2648 ccccttcttctgctgacccatggttgatctctctctctctctctctct 2707
 121 ccccttcttctgctgacccatggttgatctctctctctctctctctct 2767
 QY 2708 tactcgtctccacgcagacagaccggcgctattatggccaagaacttgcagcct 2767
 181 tactcgtctccacgcagacagaccggcgctattatggccaagaacttgcagcct 240
 DB 2768 gtttgaagaatgcctcgcagaaatgcagcttgc-agaatgcatacaagaagcgt 2826
 241 gtttgaagaatgcctcgcagaaatgcagcttgc-agaatgcatacaagaagcgt 300

RESULT 7 447 bp mRNA linear EST 18-SEP-1996
 AA057418
 LOCUS z559h03.s1 Soares retina N2B4HR Homo sapiens cDNA clone
 DEFINITION IMAGE:381269 3', mRNA sequence.
 AA057418
 ACCESSION AA057418.1 GI:1550059
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 447)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson R.
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available royalty-free through LNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40m3 fwd. from Amersham
 High quality sequence stop: 339.
 Location/Qualifiers
 1..447
 /organism="Homo sapiens"
 /db_xref="GDB:1289526"

/db_xref="taxon:9606"
 /clone="IMAGE:381269"
 /clone_1b="Soares retina N2B4HR"
 /sex="male"
 /tissue_type="retina"
 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: eye; Vector: pRT73D (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 95 a 109 c 107 g 133 t 3 others
 ORIGIN
 Query Match 10.1%; Score 285.4; DB 9; Length 447;
 Best Local Similarity 98.7%; Pred. No. 1.7e-41; Indels 1; Gaps 1;
 Matches 297; Conservative 0; Mismatches 3;

QY 2528 gtcacacagaaagaacatgcctgtctccctccgggaattctctttaagactga 2587
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 QY 2588 agtcgctgctagtggttcaattgttttttttccctctctctctctctt 2647
 61 agtcgctgctagtggttcaattgttttttttccctctctctctctctt 120
 DB 2648 ccccttcttctgctgacccatggttgatctctctctctctctctctct 2706
 121 ccccttcttctgctgacccatggttgatctctctctctctctctctct 2766
 QY 2707 gtttgaagaatgcctcgcagaaatgcagcttgc-agaatgcatacaagaagcgt 2826
 181 gtttgaagaatgcctcgcagaaatgcagcttgc-agaatgcatacaagaagcgt 240
 DB 2767 gtttgaagaatgcctcgcagaaatgcagcttgc-agaatgcatacaagaagcgt 2826
 241 gtttgaagaatgcctcgcagaaatgcagcttgc-agaatgcatacaagaagcgt 300

RESULT 8 467 bp mRNA linear EST 30-JAN-1997
 AA020992
 LOCUS z65f07.s1 Soares retina N2B4HR Homo sapiens cDNA clone
 DEFINITION IMAGE:363877 3' similar to contains Alu repetitive element; mRNA sequence.
 AA020992
 ACCESSION AA020992.1 GI:1484745
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 467)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.


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/sex="male"
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/dev_stage="55 year old"
/lab_host="DH10b (ampicillin resistant)"
/vector="Organ; eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5'
TGTTCACATCTGAAGTCGAGCGAGCGCGCGCTTTTCTTTTCTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Scores and M.Fatima Bonaldo."
96 a 96 c 104 g 117 t 6 others

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Query Match	7.0%;	Score 197;	DB 10;	Length 413;
Best Local Similarity	99.5%;	Pred. No. 1.4e-25;		
Matches 197; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 2630 cttctctctctctcttctgaccttcttagctgcaactcccaaggatcttcgccttgctc 2685
Db 1 cttctctctctcttggccctttctttaccttgacactcccaaggatcttcgccttgctc 60			

2690 tccctcgtgggtgtgtgtactcgttccacacgcacagaacccgctgcctattatggcc 2/4
 61 |||||
 mcmcmctggcgcttggctggtgactgcttccacgcgcacagaaacccggccctattatggcc 120

[illegible]

Qy	2810	gctatccaagagacgtg	2827	-
				-
Db	181	gctatccaagagacgtg	198	-

[illegible]

DEFINITION	AV715411	DCB	Homo sapiens	cdna	clone	deduced	1
ACCESSION	AV715411						
VERSION	AV715411.1	GI:10796928					
KEYWORDS	EST.						

SOURCE	ORGANISM
human.	Homo sapiens
	Chordata; Craniata; Vertebrata; Euteleostei
	Eukaryota; Metazoa;
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 696)
Xu, X., Gu, Y., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.
Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao
Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.

TITLE	16, Cheng, Z., and Han, Z.
JOURNAL	Homo sapiens cDNA DCB clones
COMMENT	unpublished (2000)
	Contact: Zeguang Han
	Professor at Shanghai

Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801932
Email: hanzg@chgc.sh.cn

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This clone is available at CHGC in Shanghai
Location/Qualifiers
1. .696
/corranism="Homo sapiens"
FEATURES
SOURCE
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DCBAUC01"
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BASE COUNT      210 a      141 c      156 g      189 t
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/note="Vector: pRiplex2; site_1: sf1A; site_2: sf1B

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Best Local Similarity	87.8%;	Pred. No. 1.8e-23;		
Matches 202;	Conservative	0;	Mismatches 28;	Indels 0;

QY 2401 taggaataagtcagcaccgaagcagtggttaagccgagagctcgaagaacggacct 2460
|||||
Db 1 TAGGAATTAAGTCAGCACCAGACAGTGTTAAGCCGAGGCTCGGAAGAACGGCACT 60

Df
61 TTTCTTCTGTAAGAACTATATGCGGGCGAATGACCTCTGGAGGCTGTATTACCCTT 120

Oy 2461 ttctcttcgcgaagaatcattgaggggcgcaatgagctctgtgagctctgtttacogct 2520

Oy	2521	tttattgtcacagaaggaacgcctgctccctcgggaatttcctcttaa	2580
Dβ	121	 tmttatgtcacacagaaaaaaanactgacctgatccccctcgsgaatctctcttta	180

Oy 2581 gactgtaagtcgcgcctgagtggttcaattctgtttgtttctctgcgc 2630
 ||||| | | | | | | | | | | | | | | | |
 Db 181 GACGCTTCTTACGTCCTGCTAGATTTCGTCNAAGTGTATGCCC 230

RESULT 15
B1838027
000 h
mpm
linear
EST 04-OCT-2001

LOCUS	BI838027	848 bp	1 clone	IMAGE:5222802.5
DEFINITION	603083875F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222802.5, mRNA sequence.			
ACCESSION	BI838027			

VERSION	BI838027.1	GI:15949577
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
NIH-MGC <http://mgc.ncl.nih.gov/>.
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHOR: National Institutes of Health, Mammalian Gene Collection (1997)
 TITLE: Unpublished (1999)
 JOURNAL: Contact: Robert Strausberg, Ph.D.
 COMMENT: Email: cgaabbs-r@mail.nih.gov

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
RNA Sequencing by: Incyte Genomics, Inc.

bioRxiv preprint doi: <https://doi.org/10.1101/156019>; this version posted November 15, 2017. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

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High quality sequence stop: 813.
Location/Qualifiers
1. .828
source
/oranidism="Homo sapiens"

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/ab_xref="taxon:9606"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"

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/note="Organ: pooled pancreas and spleen; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo

male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH-MGC Library."

BASE COUNT 253 a 181 c 194 g 200 t

ORIGIN

Query Match Best Local Similarity 6.4%; Score 181.8; DB 10; Length 828; Matches 198; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2406 aataagtcagcaccgaagcagtggttaagccggaaggctcggaagaacggacatttct 2465
 DB 1 AATAAGTCAGCACCGAAGCAGTGTTAAGCCGAGGCTCGGAGAACGGACCTTTCT 60
 QY 2466 ttctcgaaaaagtatatatggggctggaatgagctctcgaggcttgtaacgatttta 2525
 DB 61 TTCTCGAAAAAGTTATATGGGGCTGAATGAGCTTCTGAGGCTTGTTACGTTTTTA 120
 QY 2526 ttgtacacagaagaagaacgccttgctcccttcggaattctctttaagactg 2585
 DB 121 TTGTCACACAGAAAGAAAGAACTGCTGCTCCCTTCGGAATTCTCTTTAAGACTG 180
 QY 2586 taagtcgctgcctgagtggttcaatttgatttgcttctgccc 2630
 DB 181 TTCTTACGCTGTGCTAGATTATGTCCAAAAGGTAAATGCC 225

Search completed: September 7, 2002, 14:51:57
 Job time: 16216 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:26:54 ; Search time 12179.2 Seconds
(Without alignments)
4089.359 Million cell updates/sec

Title: US-09-834-291-3

Perfect score: 2380
Sequence: 1 agcttttttggtacattt.....tggtatcaagaagacgtg 2380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_hlg:*
4: gb_om:*
5: gb_om:*
6: gb_om:*
7: gb_ph:*
8: gb_ph:*
9: gb_ph:*
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32: gb_ph:*
33: gb_ph:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID

Description

1	2380	100.0	2380	6	AX026091	AX026091 Sequence
2	2380	100.0	2827	6	AX026092	AX026092 Sequence
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4	1899.6	79.8	3212	6	AX026089	AX026089 Sequence
5	1715	72.1	2344	9	HSCD955FR	HSCD955FR
6	1713.4	72.0	2165	9	HUMFAS	HUMFAS
7	1701.4	71.5	1877	9	HSAPT1	HSAPT1
8	1372.8	57.7	1608	6	AX347321	AX347321 Sequence
9	879.4	36.9	1608	6	AX347320	AX347320 Sequence
10	856.8	36.0	1608	6	AX026090	AX026090 Sequence
11	611.8	25.7	720	6	AX026090	AX026090 Sequence
12	259	10.9	398	11	G27038	G27038 SHGC-30908
13	245	10.3	2719	9	BC012479	BC012479 Homo sapi
14	216	9.1	702	9	HSAT279011	HSAT279011 Homo sapi
15	216	9.1	702	9	HSAT279012	HSAT279012 Homo sapi
16	216	9.1	702	9	HSAT279013	HSAT279013 Homo sapi
17	188.8	7.9	1728	4	BTU24240	BTU24240 Bos taurus
18	161	6.8	266	6	AX026120	AX026120 Sequence
19	161	6.8	266	6	HSAT011034	HSAT011034 Homo sapi
20	155	6.5	2551	6	ARI43111	ARI43111 Sequence
21	155	6.5	2551	6	HSAP01	HSAP01 Sequence
22	129	5.4	2471	6	HSAP01	HSAP01 Sequence
23	129	5.4	2471	6	HSAP01	HSAP01 Sequence
24	129	5.4	2471	6	HSAP01	HSAP01 Sequence
25	129	5.4	2471	6	HSAP01	HSAP01 Sequence
26	129	5.4	2471	6	HSAP01	HSAP01 Sequence
27	129	5.4	2471	6	HSAP01	HSAP01 Sequence
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30	78.6	3.3	167564	2	AF267170	AF267170 Homo sapi
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32	73.8	3.1	143584	2	AC090193	AC090193 Homo sapi
33	73.8	3.1	170261	2	AC008040	AC008040 Homo sapi
34	73.8	3.1	170261	2	AC008040	AC008040 Homo sapi
35	73.8	3.1	173387	9	AC090063	AC090063 Homo sapi
36	71.8	3.0	7218	6	AC023788	AC023788 Homo sapi
37	69.8	2.9	62999	2	AC087594	AC087594 Homo sapi
38	69.8	2.9	62999	2	AC087594	AC087594 Homo sapi
39	69.8	2.9	62999	2	AC087594	AC087594 Homo sapi
40	68.8	2.9	194183	2	AC026010	AC026010 Homo sapi
41	67.4	2.8	81117	6	AC016898	AC016898 Homo sapi
42	66.6	2.8	273413	2	AC079314	AC079314 Homo sapi
43	65.6	2.8	148069	9	AC006428	AC006428 Homo sapi
44	65.6	2.8	163951	2	AC091976	AC091976 Homo sapi
45	65	2.7	71112	2	AC102285	AC102285 Mus muscu

ALIGNMENTS

RESULT 1
AX026091 2380 bp DNA linear PAT 16-SEP-2000
LOCUS AX026091 3 from Patent DE19847779.
DEFINITION AX026091
ACCESSION AX026091
VERSION AX026091.1 GI:10187522
KEYWORDS

SOURCE

ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2380)
Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 3 03-FEB-2000;

TITLE

JOURNAL DEUTSCHES KREBSFORSCH (DE)
Location/Qualifiers

FEATURES

source
1..2380
/organism="Homo sapiens"
/db_xref="taxon:9606"

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Db	2101	GCCTTGCTCCCTCCGGAAATCTCTCTTTAAGACTGAAGTCGGTGCCTGAAGTGTT	2160
QY	2161	caattgttttcttcttcgacctctctctctctcttcttgccttcttagctgacct	2220
Db	2161	CATTGTCTTTGGTTTCTTCGCCCTTCCTCTTCTCTTTTGCCCTTCTTAGTGTGACATC	2220
QY	2221	ccatgagatcttcgcttgccttcctcgcgtctggttgcgttactgcttccaccgcacg	2280
Db	2221	CCATGCGATTTCGCTTGCTGCTCCTCCTGCTGGGTGGTGGTACTCCTTCCACCGCACAG	2280
QY	2281	aaccgcgcgacctatattgycacgaagaacttgcgcgcgctgttttgaagaagtcctcgct	2340
Db	2281	AACCGCGCGCTATTATTGGCCAAAGAACTTGAGCACCGCTGTTTGAAGAGTCCCTCGCT	2340
QY	2341	cagaatgcgcagcttcagatgcgtaactcaagaagacgtg	2380
Db	2341	CAGAAATGCCAGCTTGACAGATGCTATTCAAGAGACGTG	2380
RESULT	2		
AX026092		2827 bp	DNA
LOCUS			linear
DEFINITION	Sequence 4 from Patent DE19847779.		PAT 16-SEP-2000
ACCESSION	AX026092		
VERSION	AX026092.1	GI:10187523	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE			
AUTHORS	1 (bases 1 to 2827)		
TITLE	Mueller-Schilling M., Kramer P. and Oren M.		
JOURNAL	Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy		
	Patent: DE 19847779-C 4 03-FEB-2000;		
	DEUTSCHES KREBSFORSCH (DE)		
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Matches 2380; Conservative	0; Mismatches 0; Indels 0; Gaps 0.		
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Db	448	AGCTTTTGGCTACATTTTATTATTGTAAAGTAAGTTAATAATACACATCTACAG	507
QY	61	ggcataataataagtaagtaaggaagaatcacatatgtagtgctggttataat	120
Db	508	GGCTAATAATAGTAAGTTAAGTAAGGAAGATCCACATATGTAGTGTGCGCTTAATAA	567
QY	121	tcaactaagaagatactgatttctgtaattgcttccctcttcttctccct	180
Db	568	TCACACTCAAGAGACTGATTTGTCAATGTGCTTCCCTTTCTCTCTTCCCT	627
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JOURNAL

Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University,
Faculty of Pharmaceutical Sciences: 13-1 Takara-machi, Kanazawa,
Ishikawa 920-0934, Japan (E-mail: nakanaka@eds.p.kanazawa-u.ac.jp,
Tel:076-234-4424, Fax:076-234-4480)

FEATURES

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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS Cheng, J., Liu, C., Koopman, W. J. and Mountz, J. D.
 TITLE Characterization of human Fas gene. Exon/intron organization and promoter region
 JOURNAL J. Immunol. 154 (3), 1239-1245 (1995)
 MEDLINE 95123075
 REFERENCE 2 (bases 1 to 1608)
 AUTHORS Cheng, J.
 TITLE Direct Submission
 JOURNAL Submitted (20-OCT-1994) J. Cheng, Univ. of Alabama at Birmingham, Birmingham, AL 35294-0007, USA
 COMMENT Related sequences: M67454 and X63717.
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QY 560 ccaaacagagctccagaaagaatgtcaactgaaggaagccctgaaagatgaaactgaaact 619
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Db 367 TTGCAAGAGTGAAGTGCAGACCTTGTTGAGAGATGCCAAAGAAATACGAAACCTTTAGTG 426
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DEFINITION Sequence 2392 from Patent WO0200928.
ACCESSION AX347321
VERSION AX347321.1 GI:18495209
KEYWORDS
SOURCE
ORGANISM synthetic construct.
artificial construct.
REFERENCE
1 (sites)
AUTHORS Olek A., Piepenbrock, C. and Berlin K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 2392 03-JAN-2002;
Epigenomics AG (DE)
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ACCESSION	G27038											
VERSION	G27038.1											
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homini; Hominidae; Homo.											
TITLE	1 (bases 1 to 398)											
JOURNAL	Olivier, M. and Cox, D.R.											
COMMENT	Unpublished, Olivier, M., Cox, D.R. (2000)											

Contact: Michael Olivier, David R. Cox
Stanford University School of Medicine
4005 Miranda Ave., 2nd Fl., Palo Alto, CA 94025, USA
Tel.: (650) 325-1000


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Db      181  CTGGCAGGAGACACACCTGAGGCCCTGGCTGCCAGCGAGCTGCTCTTCTCC 240
QY      1711  cgcgg 1715
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ACCESSION AJ279011
VERSION   AJ279011.1 GI:13539238
KEYWORDS  Apo-1 Fas; CD95 antigen; CD95 gene.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE     Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
JOURNAL   Kuppers,R.
REFERENCE 2 Somatic mutations of the CD95 gene in human B cells as a
AUTHORS   side-effect of the germinal center reaction
TITLE     Muschen,M., Re,D., Brauningner,A., Wolf,J., Hansmann,M.L., Diehl,V.,
JOURNAL   Kuppers,R. and Rajewsky,K.
REFERENCE 3 Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
AUTHORS   cells
TITLE     Unpublished
JOURNAL   3 (bases 1 to 702)
REFERENCE 4 Direct Submission
AUTHORS   Muschen,M.
TITLE     Submitted (19-SEP-2000) Muschen M., Department of Immunology,
JOURNAL   Institute for Genetics, LFI E4 R705, Joseph-Steizmann-Str. 9, 50931
COMMENT   Koeln, GERMANY
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LOCUS   HSA279012
DEFINITION Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
ACCESSION AJ279012
VERSION   AJ279012.1 GI:13539240
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SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE     Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
JOURNAL   Kuppers,R.
REFERENCE 2 Somatic mutations of the CD95 gene in human B cells as a
AUTHORS   side-effect of the germinal center reaction
TITLE     Unpublished
JOURNAL   2 (bases 1 to 702)
REFERENCE 3 Muschen,M., Re,D., Brauningner,A., Wolf,J., Hansmann,M.L., Diehl,V.,
JOURNAL   Kuppers,R. and Rajewsky,K.
REFERENCE 4 Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
AUTHORS   cells
TITLE     Unpublished
JOURNAL   3 (bases 1 to 702)
REFERENCE 5 Direct Submission
AUTHORS   Muschen,M.
TITLE     Submitted (19-SEP-2000) Muschen M., Department of Immunology,
JOURNAL   Institute for Genetics, LFI E4 R705, Joseph-Steizmann-Str. 9, 50931
COMMENT   Koeln, GERMANY
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GenCore version 4.5
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Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1372.8	57.7	1608	17	Fas promoter regio
2	879.4	36.9	1608	24	Human immune syste
3	856.8	36.0	1608	24	Human immune syste
4	190.4	8.0	859	21	Human colon cancer
5	161	6.8	266	21	Human CD95 receptor
6	155	6.5	2551	21	DNA encoding a hum
7	129	5.4	2471	16	Fas-delta-TM cDNA
8	129	5.4	2471	20	Soluble Fas recept
9	129	5.4	2534	13	Human cell surface

10	129	5.4	2534	16	AAQ95297	Plasmid pF58 contg
11	129	5.4	2534	17	AA116303	hFas coding sequen
12	129	5.4	2534	19	AAV32933	Fas cDNA. Mammali
13	127.4	5.4	2534	18	AAV07002	Human Fas antigen
14	63.6	2.7	19307	17	AA175557	Shuttle vector pad
15	62.6	2.6	9972	17	AA175557	Shuttle vector pad
16	60	2.5	2435	19	AA168854	Human lung tumour
17	59.8	2.5	35100	22	AAV20441	Human c-fms oncoge
18	59.8	2.5	38258	24	AAV20441	DNA encoding COLON
19	59.2	2.5	8888	20	AAV20441	EP-892047 Seq ID 4
20	56.2	2.4	36901	20	AAV20441	Murine LOBO homolo
21	56.2	2.4	38886	20	AAV20441	Human metastasis a
22	54.8	2.3	13545	22	AAV20441	Human nervous syst
23	54.6	2.3	6172	24	AAV20441	Human metastasis a
24	54.4	2.3	8342	24	AAV20441	Human polynucleoti
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26	54	2.3	10640	21	AAV20441	Nucleotide sequenc
27	53.4	2.2	4406	22	AAV20441	Human reproductive
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37	51.6	2.2	24259	22	AAV20441	Human immune/haema
38	51.6	2.2	39380	22	AAV20441	Tumour suppressor
39	51.6	2.2	1734	22	AAV20441	Human immune/haema
40	51.4	2.2	6519	22	AAV20441	Human steroid horm
41	51.2	2.2	12669	24	AAV20441	Human nervous syst
42	51.2	2.2	16854	22	AAV20441	Human gene regulat
43	51.2	2.2	562	22	AAV20441	Human foetal liver
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ALIGNMENTS

RESULT 1	AA1734162	standard; DNA; 1608 BP.
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XX	Fas promoter region.	
XX	Fas gene promoter; apoptosis; ageing; autoimmune disease;	
XX	T-cell senescence; ss.	
XX	Homo sapiens.	
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[illegible]

Db	582	AT- <u>AAATACCAAC</u> CACTCA <u>AAAAAG</u> CGCCCGCA <u>AAAAATAT</u> CCCATTTATACAGAA	524
Qy	1400	ccctgaactcttcttaaccctgactcttcccccctccctaacccggcgcgcaagccaagttgc	145
Db	523	CCCTTACTCTCTTCGTACCCCTAACTTCTCCCTCTCCCTACCCGGCGCAACCAATATAC	464
Qy	1460	tgaatcaatggagccctcccccacacccggcggtctcccaagcaggtctctctccatcttc	151
Db	463	TAAATCAATAA <u>AAAA</u> CCCTCCCAACCCGGAAGTCCCAAGCAAACTCTTCCCATCTCTC	404
Qy	1520	ctgacacccgggggcttttcgtgagctcgctctctgactcgcgaagaagtgcacacaggt	157
Db	403	CTAACCCACCGAAACTTTTCGTAACTCGTCTATCTCCGCAAAAATTAACACAAAT	344
Qy	1580	gtccaagaagcttcctggagagtaggaagcggttaacagtgacttggctcvgagctc	163
Db	343	ATTCA <u>AAAA</u> ACGCTCTTAAAAATTA <u>AAAA</u> ACGTTTACGAATTACTTAATCAAAACCTC	284
Qy	1640	aggggcggggactctgcaacggaacacacccctgagacagccctgctcgccacagcgagct	169
Db	263	AAAAACGAACACTTAACACGAAGAACACACACCTTA <u>AA</u> ACCAACCTTAACACCAACGAATCT	224
Qy	1700	gcctctctcccgcgagcatgtaca	1724
Db	223	ACGTCTTCTCCCGGAATTATTA <u>AA</u>	199

DE	ID	RESULT	3
DE	ABL34418	ABL34418	
DE	XX	ABL34418	standard; DNA; 1608 BP.
DE	XX	ABL34418;	
DE	XX	26-MAR-2002	(first entry)
DE	XX	Human immune system associated gene	SEQ ID NO: 2391.
DE	XX		

KW antiatherosclerotic; cytosine methylation; antiasthmatic;
KW antiatherosclerotic; antihaemetic; cytosolic; noctropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmologic;
KW antihemmetic; antiarthritis; antidyslipidemic; antipsoriatic;
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.

OS Homo sapiens.
XX
XX WO200200928-A2.
XX
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PPD 03-JAN-2002.
XXX
PPF 02-JUL-2001; 2001WO-EP07537.
XX
XX 30-JUN-2000; 2000DE-1032529.
XX 01-SEP-2000; 2000DE-1043826.
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for diagnosis and treatment of diseases associated with abnormal cytosine methylation

Chemical ID, SEQ ID NO 2391; 32pp + Sequence Listing; German.

genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,

CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.
SQ Sequence 1608 BP, 398 A, 51 C, 423 G, 736 T, 0 other;

Query Match	36.0%	Score 856.8;	DB 24;	Length 1608;
Best Local Similarity	76.7%	Pred. No. 5.7e-229;		
Matches 1061; Conservative	0;	Mismatches 329;		

[illegible]

392 aagcgtgcacgcgccagggtcttctctcatgcaactaacagttctactgaagtgaacag 451

452 agacaagcctatcaacacotacaagactggtgtaagtgcagtgacagatgcaaacaca 511

512 gggtgatggaagccctcaggaggttaacctaatgatttgaagggccaacaacagc 571
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572 cagagaataatgtcacaactgagaggaacgccttgaagaaatagaacattatggcccaaacacccccccccttc
- - -
- - - gggcgacagaggaacgctttcttagagggggttaatttaatttagatttgaggggtttaaatagattt 258

632 tattaatgcttatttaaatgaattaaatatata-----
259 tagagaagaatgtctaattgaagaggagtttgaaagttagtaaaaggt 318

319 tattaaatggtattaatggttgaattaatctgggaaggagagaggttcgtacagtgag 378

379 gtagagattcgcgacgactgttaaggaatctgaattctagtgcttagttgg 438

b

439	aattgtaattgaagttagatgagttatcatccaataataatttttggtaaa	498
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499 ttatgtaaatatttaagaagtattatcgttttaagaqataagatttttaaat 558

602 gtccacaccagcaccgaaagaattacaagatctttttttaagaaaaattggccaggaaata 931
559 gtttcttagactacgaagaatttaaatgttttttaaagaaaaatttttttttttttttt

932 atgagtaacggaagacagggaagtattgtgaatgtttaatagcggggcctatgcaatt 991
619 atgagtaacggaagacagggaagtattgtgaatgtttaatagcggggcctatgcaatt

992 tggcttaagtcgttagcttgcgttccctcttgagaataaactaaggggccctccct 1051

[illegible]

1112 acgtctgtagccctcatcttgcagccacaacatggaaccccatgaatgacccmca 1171
 1113 gggcccccacacggcgaacacatllgtaattctttatatagtgttaattgttatttccaga 798

1172 agctcttctcctaaglaacccaagaattaaccaaacgctccatcccccaaa
1173 acgttttgagtttttaactgttcagtataagaatgatgaatgttaaattcgta 858

859 agtttttttttgagtgatttagtaaatagtagaaggttttgcatttagttagtgaagtagaattttc 918

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QY 1232 ggcgtctgagctccatctctctcctcaagacccctcccaactcccaagcttgagacacag 1291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 919 ggcgtttgagtttattctttcttaagaatttttaatttttaagttgagttatagtag 978
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1292 aagcctttaaagagcagagagcgcgtctcagagtcctcaacctgaagtcagacatgcca 1351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 979 aagtttttaagaagggtagagaggttcgttcagagttttatttggaagtcag-avgta 1037
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1352 ggcactgacgaagcccgagacaggaatgccattgtgcaacgacgacctgacctct 1411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1038 gttatttgtaagacggttcgagtagaagatgattattgtgtaacgagattttgttttt 1097
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1412 cctcaacctgactctccctccctccctcccgagcagcagcagcagcagcagcagcag 1471
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DB 1098 tttatttgatttttttttttttttttttttttttttttttttttttttttttttttt 1157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1472 ggcctcccaacccgagcgtctcccccagcagagcgtctcctccctccctcccaacccgag 1531
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1158 gtttttttaatttcgagcgttttttttaagcagagtttttttttttttttttttttttt 1217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1532 gctttctgagctcgtctcgtatctcgcagcagagtgacacacagtgcttccaagaagc 1591
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1218 gttttctgaggttcgttttttttttttttttttttttttttttttttttttttttttt 1277
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QY 1592 tctctggagagtgagagagcaggttttaacagtgactgtgctgagcctcagggcgagcac 1651
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1278 ttttgaggagtgagagagcaggttttaacagtgactgtgctgagcctcagggcgagcac 1337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1652 tggcagcgaacacacacacacagcagccttgctgcacagcgagcgtctctctctcc 1711
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1338 tggctcggagatattttgaggttagttgtgttttagcggaggtgttttttttttt 1397
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QY 1712 gcg 1715
    |||
DB 1398 gcg 1401
    |||

RESULT 4
AAC98177 standard; cDNA; 859 BP.
AC AAC98177;
AC XX
AC XX
DT 09-MAR-2001 (first entry)
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:187.
DE XX
DE XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytoskeletal; cardioactive; neuroprotective; vulnerary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotoxic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.
XX Homo sapiens.
XX OS
XX PN WC200055351-A1.
XX PD 21-SEP-2000.
XX PF 08-MAR-2000; 2000OWO-US05883.
XX PR 12-MAR-1999; 99US-0124270.
XX PA (HOMA-) HUMAN GENOME SCI INC.
XX PT Rosen CA, Ruben SM;
XX WPI; 2000-587534/55.
XX DR P-PSDB; AAB53420.
XX PT Colon cancer associated gene sequences, referred to as colon cancer

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PT antigens, useful for the treatment, prevention, and diagnosis of colon
XX disorders such as colon cancer -
XX Claim 1; Page 610-611; 2104pp; English.
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
XX called human colon cancer antigens, given in AAB53224 to AAB54006. The
XX human colon cancer antigens can have cytoskeletal, cardioactive, muscular;
XX neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
XX vulnerary, nephrotoxic, antiinfective and antibacterial activities, and
XX can be used in gene therapy. The colon cancer antigen polynucleotides,
XX proteins and antibodies of the proteins are useful for the prevention,
XX treatment and diagnosis of colon disorders, such as colon cancer. The
XX polynucleotides may be used in diagnostics and research, such as for
XX chromosome identification, and as hybridisation probes. The proteins
XX may also be used to prevent diseases such as neural disorders, immune
XX system disorders, muscular disorders, reproductive disorders, infectious
XX gastrointestinal disorders, wounds, renal disorders, infectious
XX diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
XX AAB54007 represent sequences used in the exemplification of the present
XX invention.
SQ Sequence 859 BP; 214 A; 219 C; 227 G; 193 T; 6 other:

Query Match 8.0%; Score 190.4; DB 21; Length 859;
Best Local Similarity 94.7%; Pred No. 1.1e-42;
Matches 197; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1508 cttcccatctctcctgacacacacagcgtttcttgtagctcgtctctgacacagag 1567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 19 cgtccgccacagcgtctcgcacccggggtttcttgtagctcgtctctgacacagag 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1568 tgacacacagtggttcaagaacgtctctgaggagtgaggaagcgtttacagtgact 1627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 79 tgacacacagtggttcaagaacgtctctgaggagtgaggaagcgtttacagtgact 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1628 ggcctgagcctcagggcgagcagcagcagcagcagcagcagcagcagcagcagcag 1687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 139 ggcctgagcctcagggcgagcagcagcagcagcagcagcagcagcagcagcagcag 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1688 ccaggcagagctgcctctctcccgag 1715
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DB 199 ccaggcagagctgcctctctcccgag 226
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RESULT 5
AAZ88700 standard; DNA; 266 BP.
ID AAZ88700;
AC AAZ88700;
AC XX
AC XX
DT 11-MAY-2000 (first entry)
DE Human CD95 receptor intron 1 fragment.
DE XX
DE XX
KW p53; CD95 receptor; human; screening; apoptosis-modulation;
KW cancer chemotherapy; ss.
XX Homo sapiens.
XX OS
XX PN DE1984779-CL.
XX PD 03-FEB-2000.
XX PF 16-OCT-1998; 98DE-1047779.
XX PR 16-OCT-1998; 98DE-1047779.

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DR	P-PSDB: AAB19341.
XX	
PT	Antisense oligonucleotides for treating hepatitis and colon, liver or
PT	lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
PT	1 (Fap-1) expression
XX	
PS	Example 2: Page 71-73; 116pp; English.
XX	
CC	The present sequence encodes human Fas (Apo-1). The specification
CC	describes antisense compounds which are targeted to the 5'-untranslated
CC	region, translational start site, translational termination region
CC	or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
CC	ligand (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine
CC	phosphatase). The antisense compounds are used to inhibit the
CC	expression of Fas, FasL or Fap-1 in cells or tissues. They are used
CC	to treat autoimmune or inflammatory diseases such as hepatitis. They
CC	can also be used to treat cancer, especially colon, liver or lung
CC	cancer or lymphoma.
XX	

	Query Match	6.5%; Score 155; DB 21;	Length 2551;
	Best Local Similarity	100.0%; Pred. NO. 1.8e-32;	
	Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1561 gcaagagtgacacacacaggtgtcttcaaaagacgcctcttgysgagtgagagcggtttacga	1620	
DB	1 gcaagagtgacacacacaggtgtcttcaaaagacgcctcttgysgagtgagagcggtttacga	60	
QY	1621 gttacttgctygagacctcagagggcgcgcaacttgycacagaaacacaccttgagcgagccc	1680	
DB	61 gttacttgctygagacctcagagggcgcgcaacttgycacagaaacacaccttgagcgagccc	120	
QY	1681 tggctgcccacggcgagagctgcctcttctccgcgg	1715	
DB	121 tggctgcccacggcgagagctgcctcttctccgcgg	155	

RESULT	7
AA093879	
ID	AA093879 standard; cDNA; 2471 BP.
XX	
AC	AA093879;
DT	06-NOV-1995 (first entry)
XX	
DE	Fas-delta-TM cDNA.
XX	
KW	Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
KW	adoptive immunotherapy; transgenic animal; ss.
OS	Homo sapiens.
XX	
PM	Key
FT	Location/Qualifiers
FT	CDS 195..1139
FT	/*tag= a
FT	sig_peptide 195..242
FT	/*tag= b
FT	mat_peptide 243..1136
FT	/*tag= c
XX	
PN	W09513701-A.
XX	
PD	26-MAY-1995.
XX	
PE	15-NOV-1994; 94WO-US13173.
XX	
PR	15-NOV-1993; 93US-0152443.
XX	
PA	(LXRB-) LXR BIOTECHNOLOGY INC.
XX	
PI	Barr PJ, Kiefer MC, Shapiro JP;

XX WPI: 1995-200120/26.
 DR P-PSDB: AAW76238.
 XX New nucleic acid encoding Fas protein without its trans-membrane region
 PT - and related vectors, transformed cells, transgenic animals, protein and
 PT antibodies, useful for control of Fas mediated apoptosis
 XX
 XX Claim 3; Fig.3-1 to 3-4; 38pp; English.
 PS
 CC mRNA was obtd. from human lymphocytes and PCR was used to make
 CC cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
 CC region) mRNA. The PCR product was ligated into pBluescript and the
 CC recombinant plasmid was used to transfect E. coli DH5-alpha cells. The
 CC insert sequence of pBluescript-Fas-delta-TM is given in AAO93879.
 SQ
 XX Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;

Query Match 5.4%; Score 129; DB 16; Length 2471;
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1587 gacgctctcggagtgagggagcggttacgagtgacttgcttgagcctcagggcg 1646
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 gacgctctcggagtgagggagcggttacgagtgacttgcttgagcctcagggcg 60
 QY 1647 ggcactggcagcgaacacacccctgagccagcctgtgctccagcgagctgctctt 1706
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 ggcactggcagcgaacacacccctgagccagcctgtgctccagcgagctgctctt 120
 QY 1707 ctccgcgcg 1715
 ||||||||
 DB 121 ctccgcgcg 129

RESULT 8
 AAX24878
 ID AAX24878 standard; DNA: 2471 BP.

AC AAX24878;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Soluble Fas receptor DNA.
 XX
 KW Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive;
 KW graft versus host disease; autoimmune disease; psoriasis;
 KW rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
 KW ss.
 XX
 OS Mammalia.

XX Key Location/Qualifiers
 FH 195..1139
 FT /*tag= a
 FT /transl_except= (pos:519..521, aa:Gly)
 FT 195..242
 FT sig_peptide /*tag= b
 FT 243..1136
 FT mat_peptide /*tag= c
 FT 2349..2354
 FT polyA_signal /*tag= d
 FT 2455..2460
 FT polyA_signal /*tag= e
 XX
 XX W09903999-A1.
 XX
 XX 28-JAN-1999.
 XX
 XX 16-JUL-1998; 98WO-US14771.
 XX
 XX 17-JUL-1997; 97US-0052829.

XX (UNMI) UNIV MICHIGAN.

XX Chen J, Nabel GJ;

XX WPI: 1999-132243/11.
 DR P-PSDB: AAW98070.

PT Inhibition of proinflammatory responses - using an agent which
 PT modulates FasL stimulation, used for treating graft versus host
 PT disease or autoimmune disease
 PT
 PS
 XX
 XX Disclosure: Fig 4B; 71pp; English.

This present sequence is a DNA clone encoding soluble Fas receptor
 (see AAW98070). The invention provides a method for inhibiting a
 proinflammatory response in a cell mixture by administering an
 immunosuppressive agent which inhibits the proinflammatory activity
 of Fas ligand (FasL). In some embodiments, FasL is coadministered
 with the immunosuppressive agent, and the cell mixture comprises
 neutrophil cells. The method can be practised in vitro, ex vivo or
 in vivo. Suitable immunosuppressive agents include antisense
 molecules that inhibit endogenous FasL expression, soluble Fas
 receptors, ribozymes that inhibit the endogenous expression of
 FasL, drugs that inhibit FasL signalling, agents that induce the
 endogenous expression of transforming growth factor (TGF)-beta,
 and polynucleotides coding for an immunosuppressive agent such as
 TGF-beta. The method can be used for treating diseases associated
 with an undesired FasL-mediated proinflammatory response, e.g.
 graft versus host disease, or an autoimmune disease such as
 systemic lupus erythematosus, rheumatoid arthritis and psoriasis.
 The invention also provides a method for identifying agents which
 modulate FasL stimulation of a proinflammatory response.

SQ Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;

Query Match 5.4%; Score 129; DB 20; Length 2471;
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1587 gacgctctcggagtgagggagcggttacgagtgacttgcttgagcctcagggcg 1646
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 gacgctctcggagtgagggagcggttacgagtgacttgcttgagcctcagggcg 60
 QY 1647 ggcactggcagcgaacacacccctgagccagcctgtgctccagcgagctgctctt 1706
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 ggcactggcagcgaacacacccctgagccagcctgtgctccagcgagctgctctt 120
 QY 1707 ctccgcgcg 1715
 ||||||||
 DB 121 ctccgcgcg 129

RESULT 9

AAQ29959
 ID AAQ29959 standard; cDNA to mRNA; 2534 BP.

XX AAQ29959;

XX 12-MAR-1993 (first entry)
 DT
 XX
 DE Human cell surface antigen.
 XX
 KW Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.
 KW
 XX Homo sapiens.
 XX
 XX

XX Key Location/Qualifiers
 FH 195..242
 FT sig_peptide /*tag= a
 FT 243..1139
 FT mat_peptide /*tag= b


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XX Key Location/Qualifiers
FH CDS 195..1201
FT /tag= a
FT /product= Fas antigen
FT sig_peptide 195..242
FT /tag= b
FT mat_peptide 243..1998
FT /tag= c
XX
XX MO9601277-A1.
XX 18-JAN-1996.
XX
XX 03-MAR-1995; 95NO-JP00349.
XX
XX 14-FEB-1995; 95JP-0025637.
XX
XX 06-JUL-1994; 94JP-0154706.
XX
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX (NTSB) JAPAN TOBACCO INC.
XX
XX Hachiya T, Noguchi J, Yonehara S;
XX
XX WPI; 1996-087635/09.
XX
XX P-PSDB; AAR92528.
XX
XX Immunoassay method for soluble Fas antigen in body fluids - for
XX diagnosis of autoimmune diseases such as rheumatoid arthritis and
XX systemic lupus erythematosus
XX
XX Example 8; Page 49-52; 124pp; Japanese.
XX
XX This sequence represents the coding sequence for the human Fas antigen
XX contained within the plasmid pCEV4/hFas. The soluble Fas antigen is
XX included in the immunoassay kit of the invention. The kit is for the
XX assay of soluble Fas antigen and contains an immobilised anti-soluble Fas
XX monoclonal antibody, as well as the standard soluble Fas antigen encoded
XX by this sequence. The assay is simple and has high accuracy, high
XX sensitivity, and is capable of assaying a number of different specimens
XX at the same time. The immunoassay is used on biological samples (such as
XX serum) and is useful for diagnosis of autoimmune diseases such as
XX rheumatoid arthritis or systemic lupus erythematosus (SLE).
XX
XX Sequence 2534 BP; 817 A; 488 C; 502 G; 727 T; 0 other;
SQ
Query Match 5.4%; Score 129; DB 17; Length 2534;
Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1587 gacgctctgggagtgaggaagcggtttagagtgacttgctgagcctcaaggcg 1646
DB 1 gacgctctgggagtgaggaagcggtttagagtgacttgctgagcctcaaggcg 60
OY 1647 gacgctggcagcaaacacccctgagccagcctgctgcctcaggcgagctgctctt 1706
DB 61 ggcactggcagcaaacacccctgagccagcctgctgcctcaggcgagctgctctt 120
OY 1707 ctccgcgcgg 1715
DB 121 ctccgcgcgg 129

```

```

XX Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;
XX CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;
XX simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;
XX prophylactic; AIDS; ss.
XX
XX Mammalia sp.
XX
XX Key Location/Qualifiers
FH CDS 195..1202
FT /tag= a
FT /product= "Fas protein"
FT sig_peptide 195..242
FT /tag= b
FT mat_peptide 243..1199
FT /tag= c
FT polyA_signal 1831..1836
FT /tag= d
XX
XX MO9835692-A1.
XX
XX 20-AUG-1998.
XX
XX 17-FEB-1998; 98NO-GB00485.
XX
XX 17-FEB-1997; 97GB-0003276.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Scream GR, Xu X;
XX
XX WPI; 1998-456867/39.
XX
XX P-PSDB; AAM49104.
XX
XX Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency
XX diseases - by interfering with interaction of Fas with Fas-ligand
XX expressed on activated CD4+ cells; e.g. cells infected with HIV
XX
XX Disclosure; Fig 10; 71pp; English.
XX
XX The present sequence represents a Fas cDNA sequence used in the
XX method of the invention. The method is concerned with reducing
XX depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)
XX cells in an immune cell population which also comprises of Fas-ligand
XX (FasL)-expressing activated CD4+ cells. It involves contacting this
XX immune cell population with an effective amount of an agent (e.g. a
XX soluble Fas-Fc fusion protein) which would interfere with the
XX interaction between Fas and FasL. Therefore, the method is useful for
XX identifying suitable agents which can reduce depletion of activated
XX Fas-expressing CD8+ TK cells in immune cell populations. Also claimed
XX is the use of the agent in the manufacture of therapeutic compositions.
XX Apoptosis of lymphocytes can be triggered by the interaction of the
XX cell surface receptor Fas and its ligand FasL. By interfering with
XX this interaction, the method described and its preparations can prevent
XX apoptosis of CD8+ TK lymphocytes caused by expression of FasL on
XX activated CD4+ cells. Such FasL-expressing activated CD4+ cells are
XX especially the result of CD4+ cell infection with an immunodeficiency
XX virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency
XX virus (SIV). The claimed prevention of apoptosis may then allow
XX maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity
XX towards the CD4+ cells infected with the infectious agent, enabling
XX treatment (prophylactic and/or therapeutic) of immunodeficiency
XX diseases e.g. AIDS.
XX
XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
SQ
Query Match 5.4%; Score 129; DB 19; Length 2534;
Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1587 gacgctctgggagtgaggaagcggtttagagtgacttgctgagcctcaaggcg 1646

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Db 16048 ccggccgctgcagctgagccatcgtacgtacgtgcagccgagcatgtacaga 16107
OY 1727 gctcgaagaatagtagtgccacgtgagccgtgcacctaagctttaggtcgtgag 1786
    |||||
Db 16108 gctcgaagaatagtagtgccacgtgagccgtgcacctaagctttaggtcgtgag 16167
    |||||
OY 1787 gggagcccggttgagagaga 1808
    |||||
Db 16168 tttaacagctgctgactggaga 16189

RESULT 15
AAT27557/C
ID AAT27557 standard; CDNA: 9972 BP.
XX AAT27557:
XX 07-AUG-1996 (first entry)
XX Shuttle vector pAdel.CBCFTRZ.
XX Adenovirus type 5; Ad5; vector: gene therapy; gene transfer;
KW helper virus; cystic fibrosis transmembrane conductance regulator;
KM CFTR; ds; cyclic.
XX Synthetic.
XX Key location/Qualifiers
FH complement (3652..3073)
FT /*tag- a
FT /rpl_type- INVERTED
FT /note- "3' adenovirus inverted terminal repeat"
FT polyA_signal complement (3887..3684)
FT CDS /*tag- b
FT complement (8622..4065)
FT /*tag- c
FT /function- CFTR gene
FT complement (9241..8684)
FT promoter /*tag- d
FT /function- CMV enhancer/beta actin promoter
FT repeat_unit complement (9611..9254)
FT /*tag- e
FT /rpl_type- INVERTED
FT /note- "5' adenovirus inverted terminal repeat"
FT repeat_unit complement (9374..9360)
FT /*tag- f
FT /function- packaging sequence PAC I
FT repeat_unit complement (9353..9340)
FT /*tag- g
FT /function- packaging sequence PAC II
FT repeat_unit complement (9311..9298)
FT /*tag- h
FT /function- packaging sequence PAC III
FT repeat_unit complement (9301..9288)
FT /*tag- i
FT /function- packaging sequence PAC IV
FT repeat_unit complement (9276..9263)
FT /*tag- j
FT /function- packaging sequence PAC V
FT
FT
XX W09613597-A2.
XX
XX PD 09-MAY-1996.
XX
XX PF 27-OCT-1995; 95WO-US14017.
XX
XX PR 28-OCT-1994; 94US-0331381.
XX
XX PA (UYPE-) UNIV PENNSYLVANIA.
XX
XX PI Chen S, Fisher KJ, Weltzman M, Wilson JM;
XX
XX DR WPI; 1996-251463/25.

```

```

XX
PT Recombinant adenovirus produced from shuttle vector and helper virus
PT - has crippled packaging function, useful for delivering
PT transgene(s) to target cells
XX
PS Example 4; Fig 7A-7H; 149pp; English.
XX
XX Shuttle vector pAdel.CBCFTR (AAT27557) comprises the adenovirus
CC cis elements needed for replication and virion encapsidation but
CC is deleted of all viral genes. It carries a CFTR gene under
CC the control of a chimeric CMV enhancer/chicken beta-actin promoter.
CC It is used with a helper virus that supplies the sequences needed for
CC a productive viral infection but which has disabled packaging function.
CC Recombinant adenovirus is produced that is characterized by high titer
CC transgene delivery to host cells and the ability to stably integrate the
CC transgene into the host cell chromosome. Such a vector can be used
CC to transfer the CFTR gene for use in cystic fibrosis gene therapy.
XX
SQ Sequence 9972 BP; 2581 A; 2362 C; 2245 G; 2784 T; 0 other;

Query Match 2.6%; Score 62.6; DB 17; Length 9972;
Best Local Similarity 65.2%; Pred. No. 2.9e-06;
Matches 92; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

OY 1668 ctgagccagccctgctgctccagcgagctgctctctcccgagcatgtacag 1727
    |||||
Db 2980 CGGCCGCTGCAGCTGGCGCATCATGACGCTACGCGACCGGAGCATGTACAG 2921
    |||||
OY 1728 ctgagaagtagtagtgccacgtgagccgtgcacctaagctttaggtcgtgag 1787
    |||||
Db 2920 CTCGAGAAGTACTAGTGGCCACGCTGGCGCTGCACCTTAGCTTGGCAGCGCGTGT 2861
    |||||
OY 1788 ggaaccccggttgagagaga 1808
    |||||
Db 2860 TTACACGCTGCTGCTGGGA 2840

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Search completed: September 7, 2002, 18:41:53
Job time: 30007 sec


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Sequence 18, Application US/08444231
Patent No. 5652210
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,231
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,443
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-444-231-18

Query Match
Best Local Similarity 5.4%; Score 129; DB 1; Length 2471;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1587 gacgtctcggagtgaggaagcggttaacagtgacttgctgagcctcagggcg 1646
Db 1 GACGCTTCTGGGAGAGGAGGAGCGGTTTACGAGTGTGCTGGAGCCTCAGGGCG 60

QY 1647 ggcactggcagcaacacacccctgagggcagccctgctgcccagggcaggtcctt 1706
Db 61 GGCACTGGCAGCAGGAGACACCTTGAGGCCAGCCCTGCTGCCAGGCGAGCTGCTCTT 120

QY 1707 ctccgcggg 1715
Db 121 CTCGGCGG 129

RESULT 3
US-08-152-443A-18
Sequence 18, Application US/08152443A
Patent No. 5663070
GENERAL INFORMATION:
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APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPIRO, JOHN P.
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,443A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1136
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243
US-08-152-443A-18

Query Match
Best Local Similarity 5.4%; Score 129; DB 1; Length 2471;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1587 gacgtctcggagtgaggaagcggttaacagtgacttgctgagcctcagggcg 1646
Db 1 GACGCTTCTGGGAGAGGAGGAGCGGTTTACGAGTGTGCTGGAGCCTCAGGGCG 60

QY 1647 ggcactggcagcaacacacccctgagggcagccctgctgcccagggcaggtcctt 1706
Db 61 GGCACTGGCAGCAGGAGACACCTTGAGGCCAGCCCTGCTGCCAGGCGAGCTGCTCTT 120

QY 1707 ctccgcggg 1715
Db 121 CTCGGCGG 129

RESULT 4
US-08-219-237B-1
Sequence 1, Application US/08219237B
Patent No. 5874546
GENERAL INFORMATION:
APPLICANT: MAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
```

ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516762
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: pCEV4
CLONE: clone PF58
FEATURE:

NAME/KEY: CDS
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2518..2523
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
US-08-219-237B-1

Query Match 5.4%; Score 129; DB 2; Length 2534;
Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1587 gacgcttcgggaggtgaggaagcggttaccagtgactgtgctgagagcctcagggcg 1646

Db 1 GACGCTTCGGGAGGTAGGGAACGGGTTTACAGTACTTGGCTGGAGCCTCAGGGGCG 60
QY 1647 gacactggcagcagacacacccctagggccagccctggtctgcccagggcgagctcctt 1706
Db 61 GGACGTGGCAGCAGAACACACCCTTAGGCGCAGCCCTGGCTGCCAGGGGAGACTCCTCTT 120
QY 1707 ctcccgcg 1715
Db 121 CTCGCCGCG 129

RESULT 5
US-08-468-560C-1
Sequence 1, Application US/08468560C
Patent No. 6270998
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shii
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 195..1202
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 195..242
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 243..1199
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1831..1836
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2352..2357
IDENTIFICATION METHOD: by similarity with known sequence or
IDENTIFICATION METHOD: to an established consensus
FEATURE:
NAME/KEY: polyA_site
LOCATION: 2518..2532

Query Match	5.4%	Score 129	DB 4	Length 2534
Best Local Similarity	100.0%	Pred. No. 2e+25		
Matches 129	Conservative 0	Mismatches 0	Indels 0	Gap 0

	Sequences	U ₁	Indels	U ₂	Gaps
Qy	1587 gacgcctctggggagtggaaggagcggttaacagtgacttggcttgagcctcagggcg				1646
Db	1 GACGCTCTGGGGAGGAGGGAAGCCGTTACAGATGACTTGCTCGAGCCTCAGGGCG				60
Qy	1647 ggcactggcaggaacacacaccccttgagggccagcccttgctcccaaggggagctccttc				1706
Db	61 GGCACCTGGCAGCAGAACACACCCCTGAGGCCAGCCTTGCTGCTCCACAGGGGAGCTCCTTT				120
Qy	1707 ctccgcgcgcg				1715
Db	121 CTCCTGGCG				129

```

US-09-180-100-16
US-09-180-100-16
Sequence 16, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAKATA, Shigeoakazu
TITLE OF INVENTION: NOVEL Pds ANTGEN DERIVATIVE
FILE REFERENCE: 1110-201P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 2534
TYPE: DNA
ORGANISM: Homo sapiens
US-09-180-100-16

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Query Match          5.4%; Score 129; DB 4; Length 2534;
Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 129; Conservative 0; Mismatch 0;

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	Conserved	U	misMatches	U	Indels	Gaps
QY	1587	gaagctctcggggagtrgagaggaagcgagtttaagagatgactgctcggagccctcaaggcg				1646
Db	1	gaagctctcggggagtrgagaggaagcgagtttaagagatgactgctcggagccctcaaggcg				60
QY	1647	ggcactgagcagcaacacacccctctggggccaagccctgctgctcccaagcggagatcctctc				1706
Db	61	ggcactgagcagcagcaacacacccctctggggccaagccctgctgctcccaagcggagatcctctc				120

QY	1707	ctccgcgcg	171
db	121	ctccgcgcg	129

RESULT 7

US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria

```

1 STATE: VA
2
3 COUNTRY: USA
4 ZIP: 22313-0299
5
6 COMPUTER READABLE FORM:
7
8 MEDIUM TYPE: floppy disk
9
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: PatentIn Release #1.0, Version #1.25
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/232,463
16 FILING DATE:
17
18 CLASSIFICATION: 435
19
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US/07/935,313
22 FILING DATE:
23
24 APPLICATION NUMBER: EP 91 114 300.6
25 FILING DATE: 26-AUG-1991
26
27 ATTORNEY/AGENT INFORMATION:
28 NAME: BENT, Stephen A.
29 REGISTRATION NUMBER: 29,768
30 REFERENCE/DOCKET NUMBER: 30472/114 IMKU
31
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (703)836-9300
34 TELEFAX: (703)683-4109
35
36 TELEX: 899149
37
38 INFORMATION FOR SEQ ID NO: 14:
39
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 7218 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45
46 IMMEDIATE SOURCE:
47
48 CLONE: pTZgpt-F15
49
50 US-08-232-463-14

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Query Match	3.0%;	Score	71.8;	DB	1;	Length	7218;
Best Local Similarity	1.9%;	Pred. No.	1.5e-09;				
Matches	7;	Conservative	238;	Mismatches	130;	Indels	0;

QY 3 cttttttgctcaatttltttattttgaagaagtttaactcaactcactcgaagg 62
 Db 1072 yy 113
 QY 63 ctataatgaatgaattagaagaagatcccaatctgagttgctgtataatc 122
 Db 1132 yy 119
 QY 123 acaactaaagatactgattttgcaatgttccttcacctttttctctctcc 182
 Db 1192 yy 125
 QY 183 ttccattcctctccctcactcctctccttcctccctcacacctttctcctct 242
 Db 1232 yy 131
 QY 243 tttaacatttttatttaataagaacttccattcttggaatgctttagaattcaaaa 302
 Db 1312 yy 1371
 QY 303 atttgcaagataatacagaagaatgccatatcacctccttaccactcttttg 362
 Db 1372 yy 1431
 QY 363 tgcctatgaatgct 377
 Db 1432 yyygtaccAAATTCT 1446

RESULT

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367

QY	720	gaataactgaaacctagtggtgttcacagtttgaaacgctacgaatcaggttcagtcagtaat	779
		::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::	
Db	1082	RRRRRRRRRRRRRRRRRRRRTTCGACAGCTCCTCGACCTCGAGCCAGCTCGAATTAATCT	1023
QY	780	gatgtcatatcccaaac	796
Db	1022	GTGACGATGCGCAAC	1006

[illegible]

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RESULT 10
US-09-427-048A-10
; Sequence 10, Application US/09427048A
; Patent No. 6203975
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
Wilson, James M.
Fisher, Krishna J.
Chen, Shu-Jen
Waltzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNPVN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-427-048A-10

Query Match
Best Local Similarity 2.7%; Score 63.6; DB 4; Length 19307;
Matches 93; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1667 cctgagccagccctgctgcccagcgagcgtgctctctcccgcgagcatgtacaga 1726
DB 16048 cggccgctgacgctgcccagcgagcgtgctctctcccgcgagcatgtacaga 1726
QY 1727 gctcgagaagtactagtgccacgtgagccgtgacacctaagctttaggtcgctgag 1786
DB 16108 gctcgagaagtactagtgccacgtgagccgtgacacctaagctttaggtcgctgag 1786
QY 1787 gggaccgcggttgagagagga 1808
DB 16168 tttaacacgtcgtgactgggaa 16189

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GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
Wilson, James M.
Fisher, Krishna J.
Chen, Shu-Jen
Waltzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,022A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNPVN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: unknown
TOPOLGY: CDNA
US-08-836-022A-3

Query Match
Best Local Similarity 2.6%; Score 62.6; DB 3; Length 9972;
Matches 92; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1668 ctgagccagccctgctgcccagcgagcgtgctctctcccgcgagcatgtacag 1727
DB 2980 cggccgctgacgctgcccagcgagcgtgctctctcccgcgagcatgtacag 1727
QY 1728 ctcgagaagtactagtgccacgtgagccgtgacacctaagctttaggtcgctgag 1787
DB 2920 ctcgagaagtactagtgccacgtgagccgtgacacctaagctttaggtcgctgag 1787
QY 1788 ggaaccgcggttgagagagga 1808
DB 2860 tttaacacgtcgtgactgggaa 2840

RESULT 12
US-09-427-048A-3/C
; Sequence 3, Application US/09427048A
; Patent No. 6203975
GENERAL INFORMATION:
APPLICANT: Trustees of the University of Pennsylvania
Wilson, James M.
Fisher, Krishna J.
Chen, Shu-Jen
Waltzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus and
Methods of Use Thereof

```


TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Vector pSE380
US-09-498-599-2

Query Match
Best Local Similarity 75.0%; Score 62.4; DB 4; Length 4476;
Matches 78; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1668 ctgaagccagcccttgctgcccagcgagctgctctctcccgagatgtaacagag 1727
DB 533 CGCGCCGCTGCGAGCTGCGCCATCGATACGCTACGCGAGCGCGACATGTACAGAG 582

QY 1728 ctcgagagtaactagtgagccagctggccgctgacctaagctt 1771
DB 583 CTCGAGAGTACTAGTGGCCAGCTGGCCGTGCGACCTTAAGCTT 626

RESULT 15
US-08-306-691B-19
Sequence 19, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: ANTISENSE
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-306-691B-19

Query Match
Best Local Similarity 2.5%; Score 59.8; DB 1; Length 35100;
Matches 115; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 87 gaagatccacatatgtagtgcgttaataacacacagagatactgattgt 146
DB 3806 GAGGTTCAGTGTAGCTGAGATCATGACACTGCACCTCCAGCGACAGAGAGACT 3865
QY 147 caatgctcttccctcttctctctctctctctctctctctctctctc 206
DB 3866 CCATGTCCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3925
QY 207 tcttctctctcccaacaccccttctctctctctctctctctctctctct 3925
DB 3926 TTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 266
QY 267 actttcatlttgaatagttttaga 293
DB 3986 TTCTTTCTTTTCTATCTTTTGA 4012

Search completed: September 7, 2002, 18:26:08
Job time: 29062 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:32:06 : Search time 13836.9 Seconds
(without alignments)
3721.275 Million cell updates/sec

Title: US-09-834-291-3
Perfect score: 2380
Sequence: 1 agctctttgtctacattt.....tgctaatcaagagacgtg 2380

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 21979536 segs, 10817449327 residues 143959072

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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27: /cgn2_6/ptodata/2/pna/US097A_COMB.seq: *
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39: /cgn2_6/ptodata/2/pna/US6000_COMB.seq: *
40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq: *
41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq: *
42: /cgn2_6/ptodata/2/pna/US6003_COMB.seq: *
43: /cgn2_6/ptodata/2/pna/US6004_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2380	100.0	2380	US-09-834-291-3	Sequence 3, Appl
2	2380	100.0	2827	US-09-834-291-10	Sequence 10, Appl
3	1923.4	80.8	45121	US-09-997-722-10	Sequence 1, Appl
4	1899.6	79.8	3212	US-09-834-291-1	Sequence 94, Appl
5	1713.4	72.0	2165	US-09-665-615B-94	Sequence 94, Appl
6	1713.4	72.0	2165	US-08-377-522-1	Sequence 1, Appl
7	1372.8	57.7	1608	US-08-377-522-1	Sequence 1, Appl
8	1372.8	57.7	1608	US-08-377-522-1	Sequence 1, Appl
9	1372.8	57.7	1608	US-08-377-522-1	Sequence 1, Appl
10	706	29.7	3814	US-60-324-185-29531	Sequence 29531, A
11	611.8	25.7	720	US-09-834-291-2	Sequence 2, Appl
12	424.2	17.8	449	US-09-404-284-674	Sequence 674, App
13	424.2	17.8	449	US-09-524-038-674	Sequence 674, App
14	319.6	13.4	458	US-09-306-3508-14682	Sequence 14682, A
15	319.6	13.4	458	US-09-909-629-3705	Sequence 3705, Ap
16	296.8	12.3	254	US-09-652-816-3367	Sequence 3367, Ap
17	244	10.3	254	US-09-652-816-3367	Sequence 3367, Ap
18	239.2	10.1	2871	US-09-552-124-8816	Sequence 4919, Ap
19	239.2	10.1	2871	US-09-717-350-4919	Sequence 2083, Ap
20	239.2	10.1	2871	US-09-726-172-2083	Sequence 5939, Ap
21	239.2	10.1	2871	US-09-726-172-2083	Sequence 5939, Ap
22	239.2	10.1	2871	US-09-726-172-2083	Sequence 5939, Ap
23	239.2	10.1	2871	US-09-726-172-2083	Sequence 5939, Ap
24	237.4	10.0	772	US-09-760-455-21	Sequence 327, App
25	237.4	10.0	772	US-09-760-455-21	Sequence 327, App
26	234.4	9.8	2641	US-60-172-373-15844	Sequence 15844, A
27	234.4	9.8	2641	US-60-172-373-15844	Sequence 1336, App
28	212.6	8.9	428	US-09-287-618-11167	Sequence 11167, A
29	190.4	8.0	859	PCT-US00-05883-187	Sequence 187, App
30	190.4	8.0	859	US-09-925-292-187	Sequence 187, App
31	190.4	8.0	2134	US-09-758-475-120	Sequence 120, App

[illegible]

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? PRIOR APPLICATION NUMBER: PCT/DE99/03343
?
? PRIOR FILING DATE: 1999-10-18
? PRIOR APPLICATION NUMBER: DE 198 47 779.1
? PRIOR FILING DATE: 1998-10-16
? NUMBER OF SEQ ID NOS: 32
? SOFTWARE: patentIn Ver. 2.1
?
? SEQ ID NO 4
?
? LENGTH: 2827
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? TYPE: DNA
? ORGANISM: Homo Sapiens
?
US-09-834-291-4

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Matches 2380;	Conservative	0;			Gaps
QY	1	acgtttttggcacaattttttatttgttaaaagatttaataatcaatcactacg	60		
DB	448	agccttttggcactctttttttatttgttaagtgatttaataatcactcactg	507		
QY	61	ggcctaatagtataagtaagtaagaagatccacatagtgagttggcgcttaaat	120		
DB	508	ggcctaatagtataagtaagtaagaagatccacatagtgagttggcgcttaaat	567		
QY	121	tcacactaagaagatactgatttgttcaattgttccttcccttttttctctcc	180		
DB	568	tcacactaagaagatactgatttgttcaattgttccttcccttttttctctcc	627		
QY	181	ccctccactctctctcccttccctctctctctccctccctccacccctttccct	240		
DB	628	ccctccactctctctcccttccctctctctctctccctccctccacccctttccct	687		
QY	241	cttttaccattttttttttaaaagaaactttccatttgtagatgttttaagattcaaa	300		
DB	688	cttttaccattttttttttaaaagaaactttccatttgtagatgttttaagattcaaa	747		
QY	301	aaatttcagagataataacagagaatgcccataaccatctctcttaccactcttt	360		
DB	748	aaatttcagagataataacagagaatgcccataaccatctctcttaccactcttt	807		
QY	361	tgtgtctatttgatgctcagatggtgtgtccacaaggctgtgcagagcccaagggtcttccat	420		
DB	808	tgtgtctatttgatgctcagatggtgtgtccacaaggctgtgcagagcccaagggtcttccat	867		
QY	421	ggcactaacagttctactctgaaggttggaacagagacagcctctcaacaccttaacaagctg	480		
DB	868	ggcactaacagttctactctgaaggttggaacagagacagcctctcaacaccttaacaagctg	927		
QY	481	gtgtgaatgtgcagtacagatgcaaaaacacagagtgatggaagcccttcagagaggttaac	540		
DB	928	gtgtgaatgtgcagtacagatgcaaaaacacagagtgatggaagcccttcagagaggttaac	987		
QY	541	ctaacctaagatttgaggggcccaaacaggtctccagaagaaaagtcaactcgagaggaagcc	600		
DB	988	ctaacctaagatttgaggggcccaaacaggtctccagaagaaaagtcaactcgagaggaagcc	1047		
QY	601	tgaaggaatgaacagtggtgcttaagcaaaaggttttaattggttatcaatggttgtaact	660		
DB	1048	tgaaggaatgaacagtggtgcttaagcaaaaggttttaattggttatcaatggttgtaact	1107		
QY	661	aattgggaagggagagaggtctgcacagtgtaggtgtgcacaggtctgtgtgagatgcgcaag	720		
DB	1108	aattgggaagggagagaggtctgcacagtgtaggtgtgtgcacaggtctgtgtgagatgcgcaag	1167		
QY	721	aatactgaaaccttaagtgtgtccaggtcgtgaacttgatccaaattaggttggaatg	780		
DB	1168	aatactgaaaccttaagtgtgtccaggtcgtgaacttgatccaaattaggttggaatg	1227		
QY	781	atgtcattatccaaacataactctgtgcaaaattatcgtctaactactaagaactatcta	840		
DB	1228	atgtcattatccaaacataactctgtgcaaaattatcgtctaactactaagaagatctcta	1287		

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QY 841 cgttccaagcaatagtgacttgaaacagtgttcaacagacacgaagaataaaga 900
Db 1288 cgttccaagcaatagtgacttgaaacagtgttcaacagacacgaagaataaaga 1347
QY 901 tttttttaaagaataatggccaggaataatgaatgaacgaaggaacgaagtaattgt 960
Db 1348 tttttttaaagaataatggccaggaataatgaatgaacgaaggaacgaagtaattgt 1407
QY 961 gaatgttaataatagctgggctatgctgatttgcttaagtgtttagcttttctc 1020
Db 1408 gaatgttaataatagctgggctatgctgatttgcttaagtgtttagcttttctc 1467
QY 1021 ttgagaataaataaataaagggccctctcttccagaagccctatgagcaacatctgac 1080
Db 1468 ttgagaataaataaataaagggccctctcttccagaagccctatgagcaacatctgac 1527
QY 1081 ttttcaataatggttaactgttccattccagaagaactgtctgtagcttccatgtagcga 1140
Db 1528 ttttcaataatggttaactgttccattccagaagaactgtctgtagcttccatgtagcga 1587
QY 1141 caaagtgaagacagccagttcaaatgtcccgcaagtcttctctgtagtgaactccagaat 1200
Db 1588 caaagtgaagacagccagttcaaatgtcccgcaagtcttctctgtagtgaactccagaat 1647
QY 1201 gccaaggtctctgtatccagagcaggaacctctgctctgtagcttccatctctcagaac 1260
Db 1648 gccaaggtctctgtatccagagcaggaacctctgctctgtagcttccatctctcagaac 1707
QY 1261 ctcccaacttcccaaggtgtgaactacagcaagaacctttagaagaagcgagggcgcgct 1320
Db 1708 ctcccaacttcccaaggtgtgaactacagcaagaacctttagaagaagcgagggcgcgct 1767
QY 1321 ctgagagtcctcacctgagtgagtgatgcacgtccagcaactgcaagaaacgcccggagacaaga 1380
Db 1768 ctgagagtcctcacctgagtgagtgatgcacgtccagcaactgcaagaaacgcccggagacaaga 1827
QY 1381 tgcacatttgtgcaacgaacacctgactctctcctcaacctgactctcctccctcctacc 1440
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QY 1441 cgcgcgagacgaagtgtgctgaatcaatgtagagccctcccaacccggcggttccccacg 1500
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QY 1501 aggtctctctccatctctctctgcaacacggcggttcttgtagtgcctctgtagtctgc 1560
Db 1948 aggtctctctccatctctctctgcaacacggcggttcttgtagtgcctctgtagtctgc 2007
QY 1561 gcaagagtacacacacaggtgttcaagaacgcttctgtagagtgtaggggaagcggttaca 1620
Db 2008 gcaagagtacacacacaggtgttcaagaacgcttctgtagagtgtaggggaagcggttaca 2067
QY 1621 gtgacttgctgagagcctcagggcgagcctgtagcaggaacacacccctgagggccagccc 1680
Db 2068 gtgacttgctgagagcctcagggcgagcctgtagcaggaacacacccctgagggccagccc 2127
QY 1681 tggctgccaagcgagagctgctctctctcccgcgacatgtataagagctgaaatgact 1740
Db 2128 tggctgccaagcgagagctgctctctctcccgcgacatgtataagagctgaaatgact 2187
QY 1741 agtggccaagctgggagcctgtaaggtttaggtgctgtagaggggaaccccggttgg 1800
Db 2188 agtggccaagctgggagcctgtaaggtttaggtgctgtagaggggaaccccggttgg 2247
QY 1801 agaaagagcggaactcctgtagcaagccctgcaagccaagccaaggtccgctcccgagc 1860
Db 2248 agaaagagcggaactcctgtagcaagccctgcaagccaagccaaggtccgctcccgagc 2307
QY 1861 cgggtgggtgagtgcgccgcccggggggcgagagagagagctgcaagcctcagaac 1920
Db 2308 cgggtgggtgagtgcgccgcccggggggcgagagagagagctgcaagcctcagaac 2367
QY 1921 agatatctgctaatcttctgtagcttctcagacgttagaataatgacacccgaagcagt 1980

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Db 2368 agatatctgctaatcttctgtagcttctcagacgttagaataatgacacccgaagcagt 2427
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Db 2428 gtttaagccggaaggtctcggaagaacggcaccttctctctcgaaagaattataggg 2487
QY 2041 gctgaatgagcttcggaaggtctgtttacaggtttttatgtgtaacacagaagaagaact 2100
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QY 2101 gctgtgtctctcccggaatctctcttgaagatgtaagtcgctgctgtaggtt 2160
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QY 2161 catttggtttgttttctgcccctctctctctctcttcttggccctttagctgacac 2220
Db 2608 catttggtttgttttctgcccctctctctctctcttcttggccctttagctgacac 2667
QY 2221 ccatgtgtattctgtgctgtctctgctggttggtgtagtactgcttccacgcagacag 2280
Db 2668 ccatgtgtattctgtgctgtctctgctggttggtgtagtactgcttccacgcagacag 2727
QY 2281 aaccggcgccattatgtggccagaagaacttgagacgacctgtttgaaagtccctgct 2340
Db 2728 aaccggcgccattatgtggccagaagaacttgagacgacctgtttgaaagtccctgct 2787
QY 2341 cagaatgccaagcttgagatgctaatcaagaagactg 2380
Db 2788 cagaatgccaagcttgagatgctaatcaagaagactg 2827

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RESULT 3
US-09-997-722-10
; Sequence 10, Application US/09997722
; GENERAL INFORMATION:
; APPLICANT: MORRIS, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-10

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Query Match 80.8%; Score 1923.4; DB 36; Length 45121;
Best Local Similarity 85.1%; Pred. No. 0;
Matches 2359; Conservative 0; Mismatches 21; Indels 393; Gaps 3;

QY 1 agcttttggctacattttttatttggtaagtaagtttaataacatcatcactg 60
Db 8441 agcttttggctacattttttatttggtaagtaagtttaataacatcatcactg 8500
QY 61 ggtcataatgataatgataagtaagagataccacatatgtggttgcgtataat 120
Db 8501 ggtcataatgataatgataagtaagagataccacatatgtggttgcgtataat 8560
QY 121 tcaactcaagaataactgattgtcaatgttcttcccttttctctcctcct 180
Db 8561 tcaactcaagaataactgattgtcaatgttcttcccttttctctcctcct 8620
QY 181 ccttcatcctcttcccttactcttctcttctccttcccaaccccttctcctct 240

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QY 2008 gcacattctcttcgcaaaaagtataatggtgctgaatgagctctggaagctgtctt 2067
Db 10841 gcaactttctcttcgcaaaaagtataatggtgctgaatgagctctggaagctgtctt 10900
QY 2068 accgtttttattatgtaacacagaaaagaaactgctgtctccctccggaattctct 2127
Db 10901 accgtttttattatgtaacacagaaaagaaactgctgtctccctccggaattctct 10960
QY 2128 cttaagaactgaatgctgctgctgagtggtttcaattgtttgtttcttctgctctct 2187
Db 10961 cttaagaactgaatgctgctgctgagtggtttcaattgtttgtttcttctgctctct 11020
QY 2188 ctctctctcttctgctctcttctgctgctgctgctgctgctgctgctgctgctg 2247
Db 11021 ctctctctcttctgctctcttctgctgctgctgctgctgctgctgctgctgctg 11080
QY 2248 ctggt 2307
Db 11081 ctggt 11140
QY 2308 actgaagcagctgttttgaagagctcctcgcgcagaaatgcaagcttgagatgctaa 2367
Db 11141 actgaagcagctgttttgaagagctcctcgcgcagaaatgcaagcttgagatgctaa 11200
QY 2368 tcaagagacgtg 2380
Db 11201 tcaagagacgtg 11213

RESULT 4

US-09-834-291-1
Sequence 1, Application US/09834291
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: P53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 3212
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match 79.8%; Score 1899.6; DB 32; Length 3212;
Best Local Similarity 84.9%; Pred. No. 0;
Matches 2348; Conservative 0; Mismatches 24; Indels 394; Gaps 4;

QY 1 agctttttgctataattttttatttgaagtaagtttaataacatcatctgactg 60
Db 448 agctttttgctataattttttatttgaagtaagtttaataacatcatctgactg 507
QY 61 ggcataataagtaagtaagtaagtaagtaagtaagtaagtaagtaagtaagtaagta 120
Db 508 ggcataataagtaagtaagtaagtaagtaagtaagtaagtaagtaagtaagtaagta 567
QY 121 tcaacacacagagatactgatttgcacatgctctccctctctctctctctctctct 180
Db 568 tcaacacacagagatactgatttgcacatgctctccctctctctctctctctctct 627
QY 181 ccttcacatct 240
Db 628 ccttcacatct 687

QY 241 cttttacattttttttaatttaaatgtaactttctctctgtaagttttgagatttcaaa 300
Db 688 cttttacattttttttaatttaaatgtaactttctctctgtaagttttgagatttcaaa 747
QY 301 aatttgcaagataataacagagagatgccaataacatctctctctctctctctctct 360
Db 748 aatttgcaagataataacagagagatgccaataacatctctctctctctctctctct 807
QY 361 tgtgtctatagaatgctcagagatgctgcaagagctgcaagagctgcaagagctgcaag 420
Db 808 tgtgtctatagaatgctcagagatgctgcaagagctgcaagagctgcaagagctgcaag 867
QY 421 ggcactaaacagctactgtaagagtggaacagagacagctcattcaacactcaagaatg 927
Db 868 ggcactaaacagctactgtaagagtggaacagagacagctcattcaacactcaagaatg 987
QY 481 gtgtgaatgcaatgcaagatgcaagatgcaagatgcaagatgcaagatgcaagatgcaag 540
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QY 541 ctactagattttgagggcccaacagctcagagaaatgtaactgagagagagcc 600
Db 988 ctactagattttgagggcccaacagctcagagaaatgtaactgagagagagcc 1046
QY 601 tgaagatgcaatgcaagatgcaagatgcaagatgcaagatgcaagatgcaagatgcaag 660
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QY 661 aattggaag 720
Db 1107 aattggaag 1166
QY 721 aacttgcaaaccttgaatgctcagagctgcaagctgcaagctgcaagctgcaagctgcaag 780
Db 1167 aacttgcaaaccttgaatgctcagagctgcaagctgcaagctgcaagctgcaagctgcaag 1226
QY 781 atgtcattatcccaacatctctctgtaaaatcattgtaaacatcctcaagagctacta 840
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QY 841 ccgtcccaagcagatgctgctgcaagctgcaagctgcaagctgcaagctgcaagctgcaag 900
Db 1287 ccgtcccaagcagatgctgctgcaagctgcaagctgcaagctgcaagctgcaagctgcaag 1346
QY 901 ttttttttaagaaatggtgccaagaaatgaatgaatgaatgaatgaatgaatgaatgaat 960
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Db 1467 ttggaataataaataagagggcctcctttcagagagccttgaagagccttgaagagccttga 1526
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QY 1201 gccaagagctcttaccacagcagagcctctgagctgagctcattctctcagagac 1260
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QY 1261 ctccccaactctccagagtgtaactacagcagagagccttgaagagcagagagcagcagc 1320
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QY 1321 ctgagagctcctacactgagatgagcatgccaagcactgcaagagcagcagcagcagcag 1380


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Db 242 cttttacatttttttaataaagaaactttctcttttggaatagtttcaagatttcaaa 301
Qy 301 aaattgcagaagataataacagagaatgcaccaataacatccctcttaaccactcttt 360
Db 302 aaattgcagaagataataacagagaatgcaccaataacatccctcttaaccactcttt 361
Qy 361 tctgtctattagaatgcacagatgtgtgcacaagagctgcacagcccgaggtctcccat 420
Db 362 tctgtctattagaatgcacagatgtgtgcacaagagctgcacagcccgaggtctcccat 421
Qy 421 ggcactaaacagcttacttgaaaggctggaacagagacaagccatataacacatacagactg 480
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Qy 481 gtcgttaagtcacagatgcacagatgcacacacagaggtatagtaaaagccctcagagagtaac 540
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Qy 541 ctaacctgatttgaggggcccaaacagagctccagaaagaaatgtcaactagagaggaagcc 600
Db 542 ctaacctgatttgaggggcccaaacagagctccagaaagaaatgtcaactagagaggaagcc 601
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Qy 1141 caacatggaacgcccagatcaaaatgcccgcgaagtctttctctgtagtaactccagcaatla 1200
Db 1142 caacatggaacgcccagatcaaaatgcccgcgaagtctttctctgtagtaactccagcaatla 1201
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Db 1202 gccaaggtctctgtlaaccagagcagagcctctgcgtctagctccattccctccaagac 1261
Qy 1261 ctcccgaactcccaaggttgaactacagacagagcctttagaagagcagagagccgagct 1320
Db 1262 ctcccgaactcccaaggttgaactacagacagagcctttagaagagcagagagccgagct 1321
Qy 1321 ctccgaagtcctcacactggaagtgagcatgccagccatgcagaaagcccgaggaacagaa 1380

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Db 1322 ctccgaagtcctcacactggaagtgagcatgccaagccaatgcaggaacgcccggagacagaa 1381
Qy 1381 tgcccatgtgtgacaacgaacacctgactcctcttccacacctgactctccctctccac 1440
Db 1382 tgcccatgtgtgacaacgaacacctgactcctcttccacacctgactctccctctccac 1441
Qy 1441 cgcgcgaacgaagctgtgtgaatcaatgagccctccccaacccggggttccccaagc 1500
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Qy 1501 aggtctccttccatcctcctctgacccacccggggtcttctgtgagctgcctgactcgc 1560
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Qy 1621 gtgactgtgagagccctcagggcgggcagctgcagcagcaacacacccctgagccagcc 1680
Db 1622 gtgactgtgagagccctcagggcgggcagctgcagcagcaacacacccctgagccagcc 1681
Qy 1681 tggctgcccagcgagagctgctcttccccggg 1715
Db 1682 tggctgcccagcgagagctgctcttccccggg 1716

RESULT 6
US-09-802-669-94
; Sequence 94, Application US/09802669
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Ras Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; PRIOR APPLICATION NUMBER: US 2001-03-09
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-802-669-94

Query Match 72.0%; Score 1713.4; DB 31; Length 2165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1714; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 agctttttgtcctaattttttatttctgtaagtaagtttaataatcatcatcactcactg 60
Db 2 agctttttgtcctaattttttatttctgtaagtaagtttaataatcatcatcactcactg 61
Qy 61 ggtcataatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 120
Db 62 ggtcataatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 121
Qy 121 tcaactcaagagatactgattgttcaatgttcccttcccttcttctcctcctcctcct 180
Db 122 tcaactcaagagatactgattgttcaatgttcccttcccttcttctcctcctcctcctcct 181
Qy 181 ccttcactccttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 240

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Db 182 cctccatctctctctcccttaccctctctctctctctccctccacaccccttctctct 241
QY 241 ctttttaaatcttttttaatttaaaatgaacttttccatttgggaatgttttagattcaaa 300
Db 242 ctttttaaatcttttttaatttaaaatgaacttttccatttgggaatgttttagattcaaa 301
QY 301 aaatttgcagaaatatacagaaatgcacataccacccctctatccactcttctt 360
Db 302 aaatttgcagaaatatacagaaatgcacataccacccctctatccactcttctt 361
QY 361 tctgtctatatagtctccagagtggtgcaagaagctggcagccagggctcttctct 420
Db 362 tctgtctatatagtctccagagtggtgcaagaagctggcagccagggctcttctct 421
QY 421 ggcactaaagctctacttgaagtggaagagagcaagcctatcaacactacaagactg 480
Db 422 ggcactaaagctctacttgaagtggaagagagcaagcctatcaacactacaagactg 481
QY 481 ggtgtaagtgcagtgacagatgcacaacagaggtgataagagcctcagaggggtaac 540
Db 482 ggtgtaagtgcagtgacagatgcacaacagaggtgataagagcctcagaggggtaac 541
QY 541 ctacactagatttgaagggcccaacagagctccagaaagaaatgtcaactgagaggaagcc 600
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QY 601 tgaaggaatgcagagtgagcttaagcaaaaggttattatgtgtattatagtggtgaatc 660
Db 602 tgaaggaatgcagagtgagcttaagcaaaaggttattatgtgtattatagtggtgaatc 661
QY 661 aattgggaagggagagagtgctgcagagtgagtgagagcttggtgacagatgcacaaag 720
Db 662 aattgggaagggagagagtgctgcagagtgagtgagagcttggtgacagatgcacaaag 721
QY 721 aatttgaagaaacttgaagtgctgcagagtgagtgagagcttggtgacagatgcacaaag 780
Db 722 aatttgaagaaacttgaagtgctgcagagtgagtgagagcttggtgacagatgcacaaag 781
QY 781 atgtcatatcaaaatacactctctgtataaattcatgttataactatacagagctata 840
Db 782 atgtcatatcaaaatacactctctgtataaattcatgttataactatacagagctata 841
QY 841 cccgttccaaagcaatagtgacttgaacagtggttccacagagcagcagaaatcaaga 900
Db 842 cccgttccaaagcaatagtgacttgaacagtggttccacagagcagcagaaatcaaga 901
QY 901 ttttttttaagaataatggcaggaataatgtgtaacagagagagaggaatgt 960
Db 902 ttttttttaagaataatggcaggaataatgtgtaacagagagagaggaatgt 961
QY 961 gaattttaaataatgaactgagagtgatagcgaattggcttaagtggttcttctc 1020
Db 962 gaattttaaataatgaactgagagtgatagcgaattggcttaagtggttcttctc 1021
QY 1021 ttgagaataataaaactaaagggccctcttccagagcctatggcgaacatctgttc 1080
Db 1022 ttgagaataataaaactaaagggccctcttccagagcctatggcgaacatctgttc 1081
QY 1081 tttttcatatgtttaaactgttccatttccagaaagtggtgagcctctcatgttcagcca 1140
Db 1082 tttttcatatgtttaaactgttccatttccagaaagtggtgagcctctcatgttcagcca 1141
QY 1141 caacatgcagagccagctcaaatatgcaccccggaagcttctctctgagtgactccagcaatta 1200
Db 1142 caacatgcagagccagctcaaatatgcaccccggaagcttctctctgagtgactccagcaatta 1201
QY 1201 gccaaggtctcttaccagagagagcttggtgagcctctcatgttcagcca 1260
Db 1202 gccaaggtctcttaccagagagagcttggtgagcctctcatgttcagcca 1261
QY 1261 ctccccaacttccaggttgaactacagcagaagcctttagaagggcagagggcggct 1320
Db 1262 ctccccaacttccaggttgaactacagcagaagcctttagaagggcagagggcggct 1321

QY 1321 ctccaggtctctacactgaagtgacatgcacagccactgcaggaagcccccggagacagaa 1380
Db 1322 ctccaggtctctacactgaagtgacatgcacagccactgcaggaagcccccggagacagaa 1381
QY 1381 tggccattgttgaacagaaacccctgaactctctccactgaacttctccctccctacc 1440
Db 1382 tggccattgttgaacagaaacccctgaactctctccactgaacttctccctccctacc 1441
QY 1441 cgcgcagagccagagtggttgaatgaatgaagccctcccaacccggcggttcccaagc 1500
Db 1442 cgcgcagagccagagtggttgaatgaatgaagccctcccaacccggcggttcccaagc 1501
QY 1501 aggtctctctccactctccctgaacccaggggcttctgtgagctcgtctctgaatcgc 1560
Db 1502 aggtctctctccactctccctgaacccaggggcttctgtgagctcgtctctgaatcgc 1561
QY 1561 gcaagagtgacacacagtggttcaaaagcctctgggagtgaggaagcgtttacga 1620
Db 1562 gcaagagtgacacacagtggttcaaaagcctctgggagtgaggaagcgtttacga 1621
QY 1621 gtagcttggtctgagagctcagagggcgagcacttgacaggaacacacactgagccagcc 1680
Db 1622 gtagcttggtctgagagctcagagggcgagcacttgacaggaacacacactgagccagcc 1681
QY 1681 tggctgcagagcgagagctgctcttctcccgcg 1715
Db 1682 tggctgcagagcgagagctgctcttctcccgcg 1716

RESULT 7
US-08-377-522-1
Sequence 1, Application US/08377522
GENERAL INFORMATION:
APPLICANT: Mountz, John D.
APPLICANT: Liu, Changdan
APPLICANT: Cheng, Jianhua
APPLICANT: Koopman, William J.
APPLICANT: Zhou, Tong
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Serlich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UOAB:034/SER
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1467..1496
US-08-377-522-1

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Query Match	57.7%;	Score 1372.8;	DB 7;	Length 1608;
Best Local Similarity	99.4%;	Pred. No. 2.1e-285;		
Matches 1388;	Conservative	0;	Mismatches 7;	Indels 1.

12

QY	320	agagaatgcccatatacatcctccttataccacttcttctgtgtlctatgtatgtcga	379
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QY	380	gagtgtgtgcacaaggtctgcacgcccaggggtctcccatatgcactaagttcactga	439
Db	67	GAGTGTGTGCACCAAGGCTGTGGACGCCAGGGGCTTCTCTATGGCACTAACAGTCTACGA	126
QY	440	aagttgaaacagagacaagcctatacaacactbaaagactgtgttaagtgcagtacag	499
Db	127	AAGTTGAAACAGACAAACAGCCTATCAACCTTACAAAGACTGGTGTAGTGCAGTACAG	186
QY	500	atgcacaacacaaaggltgattgaaagccctcaggggggtgaactaacctaggtttgaagggc	559
Db	187	ATGCAAAACACAGGGTGTGTGAAGGCCCTCAGAGAGGGTAACTTAACCTGATTTGAGGGC	246
QY	560	ccaaacagcgtcccaagaagaatgtcaacttgcagagaagccttgaaggatgcacagtgggc	619
Db	247	CCAAACAGGCTCCAGAAAGAAATGTCAACTGAGAGGAAGCCTGAAGATGAACAGTGGGC	306
QY	620	taagcaaaaggttataatgttgtattaaatgggttgaattcaatttggaaaggagagagg	679
Db	307	TAAAGCAAAAGGGTATTATATGTGTTATTAATGGGTTGAATTATTTGGAAAGGGAGAGG	366
QY	680	ttgcagaagtgaagttgcaagccttgggtgcagatgtccaaaggaalactgcgaactttagt	739
Db	367	TTGCAGAGTGAAGTGCAGACCTTGGTGGAGAGCAAGCAAAAGAAATACGAAACCTTAGTG	426
QY	740	tgtcagctctgcagactgcataccaaattcaggttcagtaagtgtcatatccaaacata	799
Db	427	TGTCCAGCTGTGMACTGCATCCAAATTCAGAGTTCAAGTTATGATGATTAATTCGAAACATA	486
QY	800	cccttcgttaaattcatgcttaactcactaagaagctatactaccgttccaaagcaatagtg	859
Db	487	CCTTCTGTAAATATCATGTGCTAAACTACCTTAAGAGCTATGTACCGTTCCAAAGCAATATG	546
QY	860	actttgaacagtgttccacagagccgaagaagattacaagatttctttaaagaagaatt	919
Db	547	ACTTTGAAACAGTGTCCACGAGACAGAAAGAAATTAACAAGATTTTTTTTTTAAAGAAAT	606
QY	920	ggccaggaataataatgaatgaagaagaagaaagtaattgtgaatgttataataatagtg	979
Db	607	GGCCAGGAATATATATGATAGTACCAAGCAAGCAAGTAATGTGAAGTTAATATATAGCTGG	666
QY	980	ggctatgcgatttggctaaatgtttagcttctgtttctcctcttgaagaataaagaatag	1039
Db	667	GGCTATGATGATTTGGCTTAAGTTGTTAGCTTTGTTTCTCTGTGAAGAAATTAAGAACTAAG	726
QY	1040	ggggccccccttttcaagaagcctatgsgcgaacatctgtacttttcatatggttaactg	1099
Db	727	GGGGCCCTCCCTTTCAAGGCCCTATATGGGCAACATCTGTACTTTTTCATATAGTTAACTG	786
QY	1100	tcaattccaaagaaagcttgttagagccttcacatgattgcagcccaacaatggaagccagtc	1159
Db	787	TCAATTCACAGGAACGTCTGTGAGCCTCTCATGTTGCAAGCCCAAGAGATGGACGCCCACTC	846
QY	1160	aaatgcccgcgaagcttctctctgtagtgaactccagcaatttagccaaggtctcttaccga	1219
Db	847	AAATGCCCCCAAGTCTTCTCTGATGACTCCAGCAATTAAGCCAAAGGCTCTGTACCA	906
QY	1220	ggcaggaactctgcctctagcttcaatctccttcaagaagctcccaaatctccaggtc	1279
Db	907	GGCAGGACCTCTGCGCTGTAGCTCCATTCTCTTCAAGACACTGCCCAACTTCCCAAGTT	966

Qy	1280	gaactaagcagaagcgtcttagaagaagcgagagcgcgctctcgaagctccactga	1339
Db	967	GAAGTAAAGCAGAAAGCCTTTATGAAGAGGACAGAGCGCGCTCTGAGAGTCTCACTGAA	1026
Qy	1340	gtgagcaltgcagccacttgtcagaagacgccccggagacagaaatggccatttgtgaacgaa	1399
Db	1027	GTCAG-ATGCCAGACCACTGCAGGAAGCCCCGGACAGAAATGCCCATTTGTGAACGAA	1085
Qy	1400	ccttgactccttctcaacccttgactctccctccctactaccgcgcgagacgaagtgc	1459
Db	1086	CCCTGACTCTTCTCAACCTGTACTTCTCCCTCTCCCTACTCCCGGCGCAGGCCAAGTTGC	1145
Qy	1460	tgaatcaatlgagccctccccaacccggaggttccccaagagagcttccctccactc	1519
Db	1116	TGAATCAATGAGACCCCTCCCAACCCGGGGGTTTCCCAAGGAAGCTTCTTCCATCTTC	1205
Qy	1520	ctgaccaccggggcttctcgttgagctcgtctctgactctcgcgcaagatgcacacagtt	1579
Db	1206	CTGACCACCGGGGCTTTTGTGAGCTCGATCTGATCTGGCCAAAGTGCACACAGGT	1265
Qy	1580	gttcaaaagcagcttcctggggagttgaaagaaagcgtttaagagtgaacttgcttggagcct	1639
Db	1266	GTTCAAAAGCAGTTTCTGGGGAGTGAAGGAAAGCGTTTACGAGTGAATTTGGCTGAGACCTTC	1325
Qy	1640	agggcgaggcacttgcacgaaacacaccccttgagccagcccttgctgcgcagcggaggt	1699
Db	1336	AGGGCGAGGCACTGCGACGAGAACACACCCTGAGGGCACCCTGCGTGGCTCCACAGCGAGCTT	1385
Qy	1700	gcctcttctccggag 1715	
Db	1386	GCTCTTCTCCCGCGG 1401	

RESULT 8
US-08-377-522C-1

GENERAL INFORMATION:

TITLE OF INVENTION: Human Fas Gene Promoter Region

CORRESPONDENCE ADDRESS:

CITY: Houston
; STREET: 8011

ZIP: 77071

MEDIUM TYPE: 3.5 inch floppy

OPERATING SYSTEM: Macintosh

```

; CURRENT APPLICATION DATA:
APPLICATION NUMBER      DATE OF BIRTH

```

FILED DATE: January 20, 1999
CLASSIFICATION: 13E

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 35,423

TELECOMMUNICATION INFORMATION:

TELEFAX: (713) 777-6908

SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid

MOLECULE TYPE: linear

IDENTIFICATION: genomic DNA

TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 bp
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIX1; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
US-08-377-522D-1

Query Match 57.7%; Score 1372.8; DB 7; Length 1608;
Best Local Similarity 99.4%; Pred. No. 2.1e-285;
Matches 1388; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

320 agagaatgccctatccatccctctccatccactctcttctgtctctatctagatcctca 379
Db 7 ACAGAGATGCCCTATACCATCTCTTATCCCACTCTTCTTGTGCTATTAATCATCTCA 66
380 gaggtgtgcaagaagcttgcagccagagctctctctcatgcaactcaactctacta 439
Db 67 GAGGTGTGCAAGAGGCTGCGACGCCAGGGTCTTCCTCATGGCACTACAGCTCTACTGA 126
440 aaggtggaacagagaacagctatcaacacacacacacacacacacacacacacacac 499
Db 127 AAGGTGGAACAGAGACACACCTATCAACCTACAGAGCTGGTGTAGTGCAGTGACAG 186
500 atgcaaacacacagagcttgcagaaagccctcagagaggttaacctaaactagattgagggc 559
Db 187 ATGCAAAACACAGAGGTATGTAAGACCTCAGAGAGGTAACTAAGATTGAGAGGC 246
560 ccaaacagagctcagagaagaattgcaactgaagagagagagagagagagagagagag 619
Db 247 CCAAACAGAGCTCCAGAGAAATGTCAACTGAGAGAGAGCCTGAAGGATGAACAGTGGGC 306
620 taagcaaaaggttactaatgttattatgaatggttgaatcctaatgagagagagagag 679
Db 307 TAAGCAAAAGGTTATTAATGTATTAATGAGGTTGAATCAATTTGGAGAGGAGAGAGG 366
680 ttgcaagtggaagtgcaagagctgtgtgagcagatgcacaaagaaactccttaagt 739
Db 367 TTGCAAGAGTGAGGTGCAAGAGCTGTGTGAGAGATGCCAAAGAAATACGAAACCTTGTAGTG 426
740 tgtcagcttgcagactgcacaaatcaggttcagtaagatgagtgcttccaaacata 799
Db 427 TGTCCAGTCTGGAACGATCCAAATTCAGGTTCAAGTAAGTGTCTATTCCAAACATA 486
800 ccttctgtaaaattatgttaactccttaagagctatccagcttccaaagcaatagtg 859
Db 487 CTTTGTGTAATTAATGTATGCTAAACTAAGAGAGTATACGCTTCCAAAGCAATAGTG 546
860 acttgaacaggttgcacagagcagaaagaattacagatttttttaagaagaatt 919
Db 547 ACTTGAACAGGTTGCACAGAGCAAGAAATTAACAAGATTTTAAAAAGAAATTT 606
920 ggcagagaaataatgagtaacagagagagagagagagagagagagagagagagagag 979
Db 607 GGCAGAGAAATATGATGATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666

QY 980 ggcatacgattggcctaagttgttagcttgtttctctcttgagaaataaaactaag 1039
Db 667 GGCATATGCGATTTGGCTTAAGTTGAGCTTTGTTTCTCTGAGAAATTAAGAACTAG 726
QY 1040 gggccctcccttccagagccctatgagcgaacacacacacacacacacacacacac 1099
Db 727 GGGCCCTCCCTTTTCAGAGCCCTATGCGCAACATCTGTACTTTTATATATGTTAACTG 786
QY 1100 tccattccaggaagctctgtgagcctctcatgttgcagccacaacatgagcagagtc 1159
Db 787 TCCATTCCAGGAACGTCGTGAGCCTCTCATGTTGAGCCACAAGATGAGACGCCAGTC 846
QY 1160 aatgcccccgaagcttctctctgagtgactccaggaatagccaaaggtctgttacc 1219
Db 847 AATGCCCGCGCAAGTCTTCTCTGAGTGAATCCAGCAATTAAGCAAGGCTCTGTACCA 906
QY 1220 ggcaggaacctgagctctgagctccatctcctcacaagaccccccacttccaggt 1279
Db 907 GGCAGGACCTCTGCGCTGAGCTCCATCTCCTTCAAGACCTCCCACTTCCAGGTT 966
QY 1280 gaactacagagaagcctttagaagaagagagagagagagagagagagagagagagag 1339
Db 967 GAACACAGCAGCAAGCCTTTAAGAAAGGCGAGAGGCGCGCTCGAGGTCCTACCTGAA 1026
QY 1340 gtgagcatgcagcaccatgcagaaagcccccagagaaatgcaattgtgcagagaa 1399
Db 1027 GTGAG-ATGCCAGGCACACTGAGAGAGAGGCGCGGAGCAAGATGCCATTTGTGACAGAA 1085
QY 1400 cccctgacctctctctccacccctgactctcccccctcctaccagcagagagcagag 1459
Db 1086 CCTGACTCTCTCTCACCCCTGACTTCCCTCCCTACCCGCGCGAGGCAAGTTG 1145
QY 1460 tgaatcaatgagacccctcccaacccagaggttcccaagagagctctctccctc 1519
Db 1146 TGAATCAATGAGAGCCCTCCCAACCCGCGCTTCCCAAGAGGCTTCCCTCC 1205
QY 1520 ctgacacagagaggttctgtgagctgctctgactcgtatctgcagagagtgacacagag 1579
Db 1206 CTGACACAGAGGCTTGTGAGCTGCTCTGATCTCGCGCAAGATGACACAGAGT 1265
QY 1580 gtcaaaagagcttctgtgagtgagagagagagagagagagagagagagagagag 1639
Db 1266 GTTCAAAAGAGCTTGTGAGGAGTGAAGGAGCGCTTACAGATGACTGTGAGAGCTC 1335
QY 1640 agggagggagcactgcagagaaacacacacacacacacacacacacacacacacac 1699
Db 1326 AGGGGCGGAGCTGSCACGGAACACACCCAGAGCCCTGCTGCCAGGCGGAGGT 1385
QY 1700 gctctctcccgag 1715
Db 1386 GCCTCTTCCCGCG 1401

RESULT 10
US-60-324-185-29531
Sequence 29531, Application US/60324185
GENERAL INFORMATION:
APPLICANT: Morris, Macdonald
APPLICANT: Lal, Preeti
TITLE OF INVENTION: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
FILE REFERENCE: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 29531
LENGTH: 3814
TYPE: DNA
ORGANISM: Homo sapiens

Search completed: September 7, 2002, 22:33:42
Job time: 43916 sec

OY 754 ctgcataccaaatcaggttcaatgaatgtcattatccaaacatactctctgaaatt 813
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Db 221 CTGCATCCAAATTCAGTTCAGTAATGATGTCAATTCACAACA-ACCTTCTGTAAAT 163
OY 814 catgctaaactactaagagctctacacgttccaaagcaatgacttgaaagtgt 873
|||||
Db 162 CATGCTAACTAGTACGAGCTACTACCTTCCAAAGCAATAG-GACTTTGAGACAGTGT 104
OY 874 tcaccagagcagcaagaatatacaagaatttttttaagaanaatt 919
|||||
Db 103 TCACCAAGACGACGAAGAATTTACAGATTTTTCGTGCGCAT 58

RESULT 15
US-09-629-14682/c
Sequence 14682, Application US/0909629
GENERAL INFORMATION:
APPLICANT: Dickson, Mark C.
APPLICANT: Dimanac, Radoje T.
APPLICANT: Jones, Lee W.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 20411-776
CURRENT APPLICATION NUMBER: US/09/909, 629
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/306,350
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 41304
SOFTWARE: PL_CT_1 Version 1.1
SEQ ID NO 14682
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
US-09-909-629-14682

Query Match 13.4%; Score 319.6; DB 34; Length 458;
Best Local Similarity 96.3%; Pred. No. 2.3e-58;
Matches 391; Conservative 0; Mismatches 9; Indels 6; Gaps 6;

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Db 457 GTGATGGAAAGCCCTCAGAGGGTAACTAGATTTGA-GGCCCAACAGCTCCA 399
OY 574 gaagaaatgtcaactgagagagagcctgaagatgaacagtggcttaagcaagggtta 633
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Db 398 GAAGAAATGTCAACTGAGAGGAGAGCCTGAAGGATGACAGT-GGCTAAGCAAGGTTA 340
OY 634 ttaattgtattatgaattgagttgaatttggaaggagagaggttgagagtgaggt 693
|||||
Db 339 TTATATGTTATTAAATGGGTTGATTAATTTGGGAAGGAGAGA-GTTGCAGAGTGAGT 281
OY 694 gcagagccttggtgagcagatgcacaagaaatactgaacactttagtgcagcttgaa 753
|||||
Db 280 GCAGAGCTTGTTGGCGATGCTCAAGGAATACGAACCTTTAG-GTGTCCAGTCTGAA 222
OY 754 ctgcataccaaatcaggttcaatgaatgtcattatccaaacatactctctgaaatt 813
|||||
Db 221 CTGCATCCAAATTCAGTTCAGTAATGATGTCAATTCACAACA-ACCTTCTGTAAAT 163
OY 814 catgctaaactactaagagctctacacgttccaaagcaatgacttgaaagtgt 873
|||||
Db 162 CATGCTAACTAGTACGAGCTACTACCTTCCAAAGCAATAG-GACTTTGAGACAGTGT 104
OY 874 tcaccagagcagcaagaatatacaagaatttttttaagaanaatt 919
|||||
Db 103 TCACCAAGACGACGAAGAATTTACAGATTTTTCGTGCGCAT 58

Mon Sep 9 09:30:38 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
September 8, 2002, 01:10:21 : Search time 1826.34 Seconds
(without alignments)
3968.636 Million cell updates/sec

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2380
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Sequence: IDENTITY: NUC
Gapop 10.0, Gapext 1.0

Scoring table: Gapop 10.0, Gapext 1.0
2036664 seqs, 1522705736 residues
4073328

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Minimum DB seq length: 2000000000
Maximum DB seq length: 1000
Minimum Match 100%

Post-processing: Minimum Match 100%

Database:

Listing first 45 summaries
Pending patents: NA, New: *
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2: /cgn2-6/ptodata/2/pna/US07_NEM_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score distribution.
and is derived by analysis of SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1923.4	80.8	45121	US-10-035-832-1262	Sequence 1262, App
2	4271.4	10.0	772	US-10-011-154-674	Sequence 674, App
3	237.4	10.0	772	US-10-011-154-674	Sequence 21, App
4	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
5	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
6	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
7	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
8	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
9	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
10	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
11	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
12	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
13	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
14	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
15	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
16	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
17	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
18	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
19	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
20	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
21	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
22	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
23	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
24	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
25	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App

US-09-834-291-3.inpu

Result No.	Score	Query Match	Length	ID	Description
1	1923.4	80.8	45121	US-10-035-832-1262	Sequence 1262, App
2	4271.4	10.0	772	US-10-011-154-674	Sequence 674, App
3	237.4	10.0	772	US-10-011-154-674	Sequence 21, App
4	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
5	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
6	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
7	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
8	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
9	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
10	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
11	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
12	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
13	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
14	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
15	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
16	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
17	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
18	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
19	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
20	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
21	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
22	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
23	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
24	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
25	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	1923.4	80.8	45121	US-10-035-832-1262	Sequence 1262, App
2	4271.4	10.0	772	US-10-011-154-674	Sequence 674, App
3	237.4	10.0	772	US-10-011-154-674	Sequence 21, App
4	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
5	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
6	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
7	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
8	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
9	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
10	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
11	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
12	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
13	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
14	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
15	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
16	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
17	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
18	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
19	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
20	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
21	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
22	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
23	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
24	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App
25	155	6.3	2551	US-10-035-832-1262	Sequence 1262, App

Page 2

[illegible]

```

RESULT 2
US-10-011-154-674/C
: Sequence 674, Application US/10011154
: GENERAL INFORMATION:
: APPLICANT: Drmanac, Radoje T.
: APPLICANT: Labat, Ivan
: APPLICANT: Stache-Crain, Birgit
: APPLICANT: Dickson, Mark C.
: APPLICANT: Jones, Lee W.
: TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
: TITLE OF INVENTION: From Various Libraries
: FILE REFERENCE: 780CIP
: CURRENT APPLICATION NUMBER: US/10/011,154
: CURRENT FILING DATE: 2001-12-06
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/524,038
: PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-13
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/404,284
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-21
: NUMBER OF SEQ ID NOS: 4670
: SOFTWARE: hy-patent.pl Version 3.1
: SEQ ID NO 674
: LENGTH: 449
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-011-154-674

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[illegible]

29 GGCACGGGA 21

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1  RESULT 3
2  US-10-211-364-477
3  ; Sequence 477, Application US/10211364
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Rosen et al.
6  ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
7  ; FILE REFERENCE: P216C1N
8  ; CURRENT APPLICATION NUMBER: US/10/211,364
9  ; CURRENT FILING DATE: 2002-08-05
10 ; PRIOR APPLICATION NUMBER: 09/760,486
11 ; PRIOR FILING DATE: 2001-01-16
12 ; PRIOR APPLICATION NUMBER: 60/179,065
13 ; PRIOR FILING DATE: 2000-01-31
14 ; PRIOR APPLICATION NUMBER: 60/180,628
15 ; PRIOR FILING DATE: 2000-02-04
16 ; PRIOR APPLICATION NUMBER: 60/214,886
17 ; PRIOR FILING DATE: 2000-06-28
18 ; PRIOR APPLICATION NUMBER: 60/217,487
19 ; PRIOR FILING DATE: 2000-07-11
20 ; PRIOR APPLICATION NUMBER: 60/225,758
21 ; PRIOR FILING DATE: 2000-08-14
22 ; PRIOR APPLICATION NUMBER: 60/220,963
23 ; PRIOR FILING DATE: 2000-07-26
24 ; PRIOR APPLICATION NUMBER: 60/217,496
25 ; PRIOR FILING DATE: 2000-07-11
26 ; PRIOR APPLICATION NUMBER: 60/225,447
27 ; PRIOR FILING DATE: 2000-08-14
28 ; PRIOR APPLICATION NUMBER: 60/218,290
29 ; PRIOR FILING DATE: 2000-07-14
30 ; Remaining prior Application data removed - See File Wrapper or PALM.
31 ; NUMBER: SEQ ID NOS: 1778
32 ; SOFTWARE: PatentIn Ver. 2.0
33 ; SEQ ID NO: 477
34 ; LENGTH: 772
35 ; TYPE: DNA
36 ; ORGANISM: Homo sapiens
37 ; FEATURE:
38 ; NAME/KEY: misc_feature
39 ; LOCATION: (593)
40 ; OTHER INFORMATION: n equals a,t,g, or c
41 ; FEATURE:
42 ; NAME/KEY: misc_feature
43 ; LOCATION: (594)
44 ; OTHER INFORMATION: n equals a,t,g, or c
45 ; FEATURE:
46 ; NAME/KEY: misc_feature
47 ; LOCATION: (704)
48 ; OTHER INFORMATION: n equals a,t,g, or c
49 ; US-10-211-364-477

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[illegible]

Query Match	6.58;	Score 155;	DB 7;	Length 2551
Best Local Similarity	100.08;	Pred. No. 3.2e-23;		

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RESULT 10
US-10-035-832-1259
: Sequence 1259, Application US/10035832
: GENERAL INFORMATION:
: APPLICANT: Morris, David
: APPLICANT: Engelhard, Eric
: TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
: FILE REFERENCE: A-71249/RMS/DCf
: CURRENT APPLICATION NUMBER: US/10/035, 832
: CURRENT FILING DATE: 2002-07-22
: PRIOR APPLICATION NUMBER: US 09/747, 377
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US 09/798, 586
: PRIOR FILING DATE: 2001-03-02
: NUMBER OF SEQ ID NOS: 1613
: SOFTWARE: patentln version 3.1
: SEQ ID NO 1259
: LENGTH: 55996
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: misc_feature

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RESULT 11
US-10-027-632-145670/C
Sequence 145670, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: 2002-04-30
PRIOR FILING DATE: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363

[illegible]

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RESULT 12
US-10-113-872-796/c
; Sequence 796, Application US/10113872
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113.872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 796
; LENGTH: 2435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-113-872-796

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Best Local	Matches	81	Conservative	0	Mismatches	35
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					Gaps	0
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Db	2434	TTTTTTTTTTTTTTTTTTTTTTTTTTAAATTAATTAACCTTTATTTTGGAAATGATAC	2375			
QY	289	tagagattccaaaaaattgcagagataatacagagaatgcgcataatcacatcc	344			
Db	2374	TAGATTTCACAGAGAGTTGCAGAGATTAAGTAAAGAGATTCCTGATACCTTCAC	2319			

RESULT 13
US-10-113-872-1669/C
Sequence 1669, Application US/10113872
GENERAL INFORMATION:
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Sleath, Paul R.

Qy	250	ttttttattcaatgaacttllcatlittggaatagtlitttaggtttccaataattgca	309
Db	44	ttgtttatttcaatgaacttllcatlittgaatagtlitttaggtttcaagaagaattgca	100
Qy	310	ggagataacacagagaatgcccatatacc	337

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Search completed: September 8, 2002, 01:12:00
Job time: 37198 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:36 ; Search time 8462.63 Seconds
(without alignments)
3795.836 Million cell updates/sec

Title: US-09-834-291-3
Perfect score: 2380
Sequence: 1 agcttttgcctacattt.....tgctaatcaagagacgtg 2380

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 674847542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_lin:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465.4	19.6	467	9	AA704610 zj19h02.s
2	438.4	18.4	793	10	BT763679 603049567
3	298.4	12.5	603	9	AA058563 zif5b04.s
4	294.4	12.4	577	9	AA056275 zif5g03.s
5	286.4	12.0	442	9	AA011028 zc34d02.s
6	285.4	12.0	547	9	AA047220 zf49e11.s
7	285.4	12.0	447	9	AA057418 zf59f03.s
8	276.4	11.6	467	9	AA020992 zc65f07.s
9	270	11.3	376	9	AA020992 zc65f07.s
10	259	10.9	398	10	H86126 y994g08.s1
11	254.4	10.7	297	9	AA018441 zc50808.s
12	253.4	10.7	381	10	H86544 yf04f01.s1
13	197	8.3	419	10	R85827 yq22g10.s1
14	185.2	7.6	696	9	AV715411 AV715411
15	181.8	7.6	828	10	BT838027 603083875
16	161	6.8	429	9	AW239285 x838d02.y
17	145.6	6.1	1339	10	BG288747 60238556

18	124.2	5.2	300	9	AU100132	AU100132
19	117	4.9	932	9	AL542093	AL542093
20	105.4	4.4	1052	10	BM455788	BM455788
21	96	4.0	285	10	BM090262	BM090262
22	85	3.6	899	9	AL540709	AL540709
23	72	3.0	506	10	BG659530	BG659530
24	70.6	3.0	1101	12	CNS00396	CNS00396
25	65	2.7	286	10	B1029879	B1029879
26	64.6	2.7	343	10	B1045052	B1045052
27	64.6	2.7	169	10	B1045083	B1045083
28	64	2.7	205	10	BG998195	BG998195
29	64	2.7	267	10	BG97854	BG97854
30	64	2.7	1027	12	CNS01607	CNS01607
31	63.8	2.7	306	9	AA668797	AA668797
32	63.6	2.7	316	10	B1004597	B1004597
33	63.6	2.7	549	9	AA521324	AA521324
34	63.6	2.7	583	9	AA521406	AA521406
35	63.6	2.7	280	10	BG998167	BG998167
36	63.4	2.7	275	10	B1005814	B1005814
37	63	2.6	276	10	BG015436	BG015436
38	63	2.6	279	10	BG978282	BG978282
39	63	2.6	287	10	BF759346	BF759346
40	63	2.6	319	10	B1028532	B1028532
41	63	2.6	987	10	CNS016F1	CNS016F1
42	62.8	2.6	1101	12	CNS017XW	CNS017XW
43	62.8	2.6	613	12	AZ363784	AZ363784
44	62.6	2.6	185	10	B1009341	B1009341
45	62.4	2.6				

ALIGNMENTS

RESULT 1
AA704610 467 bp mRNA linear EST 24-DEC-1997
LOCUS zj19h02.s1 Scores: fetal_liver_spleen, lnfls_S1 Homo sapiens cDNA
DEFINITION clone IMAGE:450771 3', mRNA sequence.

ACCESSION AA704610
VERSION AA704610.1 GI:2714528
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 467)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kitzman, D., Kuwaba, T., Lacy, M., Le, N., Lennon, G., Marita, M., Martin, J., Moore, B., Schellenberg, R., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE Unpublished (1997)
JOURNAL Washington University School of Medicine
COMMENT Contact: Wilson RK
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

FEATURES
source
1.467
/organism="Homo sapiens"
/db_xref="GDB:1387127"
/db_xref="taxon:9606"
/clone="IMAGE:450771"
/clone_lib="Soares, fetal_liver_spleen, lnfls_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

Query Match	12.08;	Score 286.4;	DB 9;	Length 442;
Best Local	99.08;	Pred. NO. 3.2e-41;		
Similarity				

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/db_xref="db:1288557"
/db_xref="taxon:9606"
/clone="IMAGE:380300"
/clone_id="Soares retina N2b4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: eye; Vector: pUT73b (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

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BASE COUNT 131 a 128 c 125 g 158 t 5 others

ORIGIN

Query Match 12.0% Score 286.4; DB 9; Length 547;
Best Local Similarity 99.3%; Pred. No. 3.1e-41;
Matches 298; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 2081 gtccacagaaagaactgctgtctccctccggaattctcttaagaactgta 2140
|||||
Db 1 gtccacagaaagaactgctgtctccctccggaattctcttaagaactgta 60

Oy 2141 agtcgctgcctgagtggttcaattgtttgtcttccctctctctctt 2200
|||||
Db 61 agtcgctgcctgagtggttcaattgtttgtcttccctctctctctt 120

Oy 2201 ccccttcttgctgctgctccatggtatctctgctgctctctggtggtg 2260
|||||
Db 121 ccccttcttgctgctgctccatggtatctctgctgctctctggtggtg 180

Oy 2261 taccgttccacacagacagaccgagcctatattgccaagaactggaagcct 2320
|||||
Db 181 taccgttccacacagacagaccgagcctatattgccaagaactggaagcct 240

Oy 2321 gttttgaagaagtcctgctcagaatgcagcttgc-agaatgctaaagaagcgt 2379
|||||
Db 241 gttttgaagaagtcctgctcagaatgcagcttgc-agaatgctaaagaagcgt 300

RESULT 7 447 bp mRNA linear EST 18-SEP-1996
AA057418
LOCUS Z159h03.s1 Soares retina N2b4HR Homo sapiens cDNA clone
DEFINITION IMAGE:381269 3', mRNA sequence.
ACCESSION AA057418
VERSION AA057418.1 GI:1550059
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 447)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marks,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
JOURNAL COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 339.
Location/Qualifiers
1..447
/organism="Homo sapiens"
/db_xref="GDB:1289526"

BASE COUNT 95 a 109 c 107 g 133 t 3 others

ORIGIN

Query Match 12.0% Score 285.4; DB 9; Length 447;
Best Local Similarity 98.7%; Pred. No. 4.8e-41;
Matches 297; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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|||||
Db 1 gtccacagaaagaactgctgtctccctccggaattctcttaagaactgta 60

Oy 2141 agtcgctgcctgagtggttcaattgtttgtcttccctctctctctt 2200
|||||
Db 61 agtcgctgcctgagtggttcaattgtttgtcttccctctctctctt 120

Oy 2201 ccccttcttgctgctgctccatggtatctt-gctgtgctcctgctggtggtg 2259
|||||
Db 121 ccccttcttgctgctgctccatggtatctt-gctgtgctcctgctggtggtg 180

Oy 2260 gttactgttccacacagacagaccgagcctatattgccaagaactggaagcct 2319
|||||
Db 181 gttactgttccacacagacagaccgagcctatattgccaagaactggaagcct 240

Oy 2320 tgtttgaagaagtcctgctcagaatgcagcttgcagatgctaaagaagcgt 2379
|||||
Db 241 tgtttgaagaagtcctgctcagaatgcagcttgcagatgctaaagaagcgt 300

Oy 2380 g 2380
Db 301 g 301

RESULT 8 467 bp mRNA linear EST 30-JAN-1997
AA020992
LOCUS z665f07.s1 Soares retina N2b4HR Homo sapiens cDNA clone
DEFINITION IMAGE:363877 3' similar to contains Alu repetitive element., mRNA
sequence.
ACCESSION AA020992
VERSION AA020992.1 GI:1486745
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 467)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bernaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marks,M.

FEATURES
source

Oy	2351	agcttcgagatgcctaatacaagaacacgtc	2380
Db	241	AGCTTCGACATGGCTAATCAAGACACGTG	270
RESULT	10		
H86126			
LOCUS		398 bp	Linear EST 21-NOV-1995
DEFINITION		ys94g08.s1 Soares retina N25HR Homo sapiens	cDNA clone
ACCESSION		IMAGE:222494 3'	mRNA sequence.
VERSION		H86126	
KEYWORDS		H86126.1 GI:1067705	
SOURCE		EST.	
ORGANISM		human.	
REFERENCE		Homo sapiens	
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 398) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,J., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston ,R., Williamson,A., Wohlschlag,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995)	
TITLE		Contact: Wilson RK	
JOURNAL		Washington University School of Medicine	
COMMENT		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu High quality sequence stops: 378 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNLN ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert length: 925 Std Error: 0.00 Seq primer: Promega -21ml3 High quality sequence stop: 378. Location/Qualifiers 1..398 /organism="Homo sapiens" /db_xref="GDB:3851225" /db_xref="taxon:9606" /clone="IMAGE:222494" /clone_lib="Soares retina N25HR" /sex="male" /tissue_type="retina" /dev_stage="55 year old" /lab_host="DH10B (ampicillin resistant)" /note="Organ: eye; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTAACCAATCGATGCAGTGGAGCGGCCGCTTTTATTATTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. library constructed by Bento Soares and M.Fatima Bonaldo."	
BASE COUNT		74 a 93 c 105 g 125 t	1 others
ORIGIN			
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Db	181	GCGGCTATTATATGGCCAGAAMAACCTGAGGAGGCCTGTTTGAAAAGTCCCTCGTCAAGA	240
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ACCESSION	AA018441		
VERSION	AA018441.1	GI:1481696	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 297) Hillier,L., Clark,N., Dubucq,T., Elliston,K., Hawkins,M., Holman M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston R., Williamson,A., Wohlmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M3 fwd. from Amersham High quality sequence stop: 244.		
TITLE	Location/Qualifiers		
JOURNAL	1. .297		
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BASE COUNT	59 a 78 c 62 g 98 t		
ORIGIN			

male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 253 a 181 c 194 g 200 t

ORIGIN

Query Match

Best Local Similarity 7.6%; Score 181.8; DB 10; Length 828;
Matches 198; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Db 1 AATTAAGTCAGCACCGAAGCAGTGTAAAGCCGAGGCTCGAAGAGCGCACCTTTTCr 60
Qy 2019 ttctcgaaaaagtatatatggggctgaatgaagctctcgagcctgtttacgtttta 2078
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Search completed: September 7, 2002, 14:51:47
Job time: 16206 sec

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OY	526	ctcttctcttcttttgcaccttcttaagcttgcacttgcacatggtatcttgcgtctcc	585
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AX026092	PAT 16-SEP-2000
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 2827)	
Mueller-Schilling,M., Krammer,P. and Oren,M.	
Novel receptor dna useful for identifying apoptosis-modulating	
substances potentially useful for cancer chemotherapy	
Patent: DE 19847779 C 4 03-FEB-2000;	
DEUTSCHES KREBSFORSCH (DE)	
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ORIGIN	

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VERSION	AX026120
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REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 266)
TITLE	Mueller-Schilling,M., Krammer,P. and Oren,M.
JOURNAL	Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
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Y	2213	AAGCTTTAGGGTCGCTGGAGGGGGACCCCGGTGGAGAGAGAGACCGAACTCCTGGACAA	2272		
Y	166	ggccctgaacaagccaagccaagaagtccgctccggcgcggttgagttgctgcgcgcgcc	225		
b	2273	GCCTGCAACGCCCAAGCCAAAGGTCGCTCGCGCGCGGGGGGTGAOTGCGCGCGGCC	2332		
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QY	61	gaagttggccgtggggggcgagcaagaaattgaagcggaagcttgggaaagctttaggttcgc	120	
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RESULT	
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LOCUS	
DEFINITION	HSA279012 702 bp DNA linear PRI 02-APR-2007
ACCESSION	Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
VERSION	1.2 polymorphic allele (+275).
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ACCESSION	AJ279011
VERSION	AJ279011.1 GI:13539238
KEYWORDS	Apo-1 Fas; CD95 antigen; CD95 gene.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 702) Muschen,M., Re,D., Jungnickel,B., Diehl,V., Rajesky,K. and Kuppers,R. Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 702)
AUTHORS	Muschen,M., Re,D., Brauningger,A., Wolf,T., Hansmann,M.L., Diehl,V., Kuppers,R. and Rajesky,K. Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg cells
TITLE	Unpublished
JOURNAL	3 (bases 1 to 702)
REFERENCE	Muschen,M.
AUTHORS	Direct Submission
TITLE	Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stellzmann-Str. 9, 50931 Koeln, GERMANY
JOURNAL	Related sequences: D31968 X89101 AJ279012 AJ279013. Location/Qualifiers
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DEFINITION	Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon 1, polymorphic allele (+337).				
ACCESSION	AJ279013	GI:13539242			
VERSION	AJ279013.1				
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Muschen, M., Re, D., Jungnickel, B., Diehl, V., Rajewsky, K. and Kupfers, R.				
TITLE	Somatic mutations of the CD95 gene in human B cells as a side-effect of the germinal center reaction				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 702)				
AUTHORS	Muschen, M., Re, D., Brauningner, A., Wolf, J., Hansmann, M.L., Diehl, V., Kupfers, R. and Rajewsky, K.				
TITLE	Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg cells				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 702)				
AUTHORS	Muschen, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-SEP-2000) Muschen M., Department of Immunology, Institute for Genetics, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931 Koeln, GERMANY				
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QY	61 gaaggtaggcgttggyggggcgagacaatttgaagcggaaagcttggaagctttaagttccc 120 	
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QY	121 ttgagggggagccccggttgtgaagagaga 148 	
Db	675 TGGAGGGGGACCCCGGTGTGAGAGAGA 702	
RESULT 12		
HUMFAS	2165 bp DNA linear	PRI 14-APR-2000
LOCUS	Human DNA for Fas antigen, promoter region.	
DEFINITION	D31968	
ACCESSION	D31968.1 GI:961455	
VERSION	Fas antigen.	
KEYWORDS	Homo sapiens blood DNA, clone pF7.	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Hominidae; Homo.	
REFERENCE	1 (bases 1 to 2165)	
AUTHORS	Wada,N., Matsumura,M., Ohba,Y., Kobayashi,N., Takizawa,T. and Nakanishi,Y.	
TITLE	Transcription stimulation of the Fas-encoding gene by nuclear factor for interleukin-6 expression upon influenza virus infection	
JOURNAL	J. Biol. Chem. 270 (30), 18007-18012 (1995)	
MEDLINE	95355401	
REFERENCE	2 (bases 1 to 2165)	
AUTHORS	Nakanishi,Y.	
TITLE	Direct Submision	
JOURNAL	Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa, Ishikawa 920-0934, Japan (E-mail:nakanaka@ds.p.kanazawa-u.ac.jp, Tel:076-234-4424, Fax:076-234-4480)	
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	276..284	
	/bound_moiety="NF-II6"	
	481..489	
	/bound_moiety="NF-II6"	
	772..780	
	protein_bind	

[illegible]

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/chromosome="1"
/clone="LJ03H13"
/clone_lib="LJT_library"
/note="TM0012b, a part of TAC clone: TM0012"
BASE COUNT      13734 a   7633 c   6945 g   13508 t
ORIGIN
Query Match              6.6%; Score 47.6; DB 8; Length 41820;
Best local Similarity    58.6%; Pred. No. 0.56; 69; Indels 3; Gaps 1
Matches 102; Conservative 0; Mismatches
QY  402 ttgtttaccgcttattatgctacacagagaagaaactgcctgctccctccggga 461
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Db  29637 TTGTTTTCTCTCTTTACTTACCAACAGCAATAATTAATAAACAATTTCCTAAATGA 29578
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QY  462 ttctctccttaaacgaactgaagtcgcgcgcgcgaagtgttcaatttggttg 518
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QY  519 tgacctctctctctctctctctttgccccttttagcttgcaatcccatggtgat 572
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```

1. 1. 1.

WPI; 2001-514838/56.

XXX
XX
Tang YT
Ting
Dennis

DR	P-PSDB; AAO04192.
XX	
PT	Isolated nucleic acids and polypeptides, useful for preventing
PT	diagnosing and treating e.g. leukaemia, inflammation and immune
XA	disorders -
PS	
XX	Claim 1; SEQ ID NO 4183; 1399pp + Sequence Listing; English.
CC	
CC	The invention relates to human polynucleotides (AI79941-AI93841) and
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC	cytokine, cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC	peptide therapy. The polypeptides have various cytokine-like activities,
CC	e.g. stem cell growth factor activity, haematopoiesis regulating
CC	activity, tissue growth factor activity, immunomodulatory activity and
CC	activin/inhibin activity and may be useful in the diagnosis and/or
CC	treatment of cancer, Leukaemia, nervous system disorders, arthritis and
CC	Inflammation.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 428 BP; 203 A; 48 C; 92 G; 82 T; 3 other;
Query Match	6.7%; Score 48.4; DB 22; Length 428;
Best Local Similarity	54.2%; Pred. No. 0.0006;
Matches 97; Conservative 0; Mismatches 82; Indels 0; Gaps 0;	
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OY	472 aagactgtaagtcgcgtcgtagtggttcatttgtttgttttcgccctctt 531
Dd	
OY	221 ttttttttatgcccccccctcttttttttttttttttttttttttttttt 162
Dd	
OY	532 ctctcttgcccttcttacctgcaccatcgatcttcgctgctgcctgctg 590
Dd	
OY	161 ttcnctgtg 103
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DT	06-NOV-2001 (first entry)
DE	
Human polynucleotide SEQ ID NO 11295.	
XX	
Human; cytokine; cell proliferation; cell differentiation; gene therapy;	
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorders; arthritis; inflammation; ss.
OS	
Homo sapiens.	
WO200164835-A2.	
PN	
WO200164835-A2.	
XX	
07-SEP-2001.	
PD	
26-FEB-2001; 2001WO-US04927.	
PPF	
28-FEB-2000; 2000US-0515126.	
EPR	
18-MAY-2000; 2000US-0577409.	
XX	
PA	
(HYSE-) HYSEQ INC.	
XX	

[illegible]

XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPT: 2001-514838/56.
XX P-PSDB; AAO002346.
DR
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
PS
XX
XX Claim 1: SEQ ID NO 2337; 1399PP + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhbin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 386 BP; 213 A; 30 C; 52 G; 72 T; 19 other;
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					Gaps
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Db	173	ttttttttaaaccctcccccctcccnnttttttttttttttttttttttttttttt	114		
Oy	532	ctctcttttgcctcttctagcttgacatcccaatgagatttcgttgctgcctcg	587		
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XX	06-NOV-2001	(first entry)			
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XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;				
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;				
KM	tissue growth factor; immunomodulatory; cancer; leukaemia;				
XX	nervous system disorders; arthritis; inflammation; ss.				
XX					
OS	Homo sapiens.				
PN	W0200164835-A2.				
PD	07-SEP-2001.				
XX					
XX	26-FEB-2001; 2001MO-US04927.				
PF					
XX	28-FEB-2000; 2000US-0515126.				

KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 XX nervous system disorders; arthritis; inflammation; ss.
 OS Homo sapiens.
 XX WO200164835-A2.
 PN 07-SEP-2001.
 PD 26-FEB-2001; 2001WO-US04927.
 PF 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 DR WPI; 2001-514838/56.
 DR P-PSDB; AA009253.
 XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX Claim 1; SEQ ID NO 9244; 1399pp + Sequence Listing; English.
 PS The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC Sequence 420 BP; 204 A; 73 C; 65 G; 75 T; 3 other;
 SQ

Query Match
 Best Local Similarity 5.7%; Score 41.2; DB 22; Length 420;
 Matches 97; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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 ID AAS44777 standard; DNA; 424 BP.
 XX AAS44777;
 XX
 XX 18-DEC-2001 (first entry)
 DT

XX Human contig polynucleotide sequence #30.
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 XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
 KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
 KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
 KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
 KW cytoskeletal; antineoplastic; antiarthritic; vulnery; antineoplastic;
 KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
 KW neuroprotective; osteopathic; antidiabetic; antisthmatic; antiallergic;
 KW immunostimulant; analgesic; gene therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200164834-A2.
 PN 07-SEP-2001.
 PD 26-FEB-2001; 2001WO-US04926.
 PF 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 PR 17-JUN-2000; 2000US-0597707.
 PR 14-JUL-2000; 2000US-0616807.
 PR 19-SEP-2000; 2000US-0664641.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 PI Drmanac R;
 DR WPI; 2001-589862/66.
 DR P-PSDB; AAU2877.
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis, treatment of
 PT cancer, neurological, inflammatory disorders and for use in arrays for
 PT detection -
 XX Claim 1; SEQ ID NO 374; 153pp; English.
 PS Sequences AAS44576-AAS44919 represent full-length polynucleotides and
 XX contig polynucleotides encoding polypeptides of the invention. The DNA
 CC and protein sequences are useful for the treatment, diagnosis and
 CC prevention of various types of disorder in a mammalian subject such as a
 CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
 CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
 CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, anyotrophic lateral sclerosis, spinal muscular atrophy and
 CC Menckie disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 CC in culture or to give rise to neuroepithelial cells that can be used to
 CC disorders. The sequences may also be used for regeneration of bone,
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 CC Sequence 424 BP; 138 A; 60 C; 110 G; 110 T; 6 other;
 SQ

Query Match
 Best Local Similarity 5.7%; Score 40.8; DB 22; Length 424;
 Matches 97; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0, Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	44	6.1	7218	1	Sequence 14, Appl
3	38.4	5.3	3133	1	Sequence 1, Appl
4	37.8	5.2	257	2	Sequence 24, Appl
5	37.4	5.2	72604	4	Sequence 7, Appl
6	37.4	5.2	123	4	Sequence 1, Appl
7	37.2	5.2	123	4	Sequence 1, Appl
8	36.6	5.1	4743	3	Sequence 16, Appl
9	36.6	5.0	152331	3	Sequence 14, Appl
10	35.4	4.9	372	4	Sequence 13, Appl
11	35.4	4.9	3168	2	Sequence 14, Appl
12	35.2	4.9	3168	2	Sequence 14, Appl
13	35.2	4.9	3168	2	Sequence 14, Appl
14	35.2	4.9	10163	2	Sequence 1, Appl
15	35.2	4.9	10163	2	Sequence 1, Appl
16	35.2	4.9	10163	2	Sequence 1, Appl
17	35.2	4.9	10163	2	Sequence 1, Appl
18	34.6	4.8	289	4	Sequence 17, Appl
19	34.6	4.8	289	4	Sequence 17, Appl
20	34.6	4.8	291	1	Sequence 7, Appl
21	34.6	4.8	291	1	Sequence 7, Appl
22	34.6	4.8	291	1	Sequence 7, Appl
23	34.6	4.8	291	1	Sequence 7, Appl
24	34.6	4.8	291	1	Sequence 7, Appl
25	34.6	4.8	291	1	Sequence 7, Appl
26	34.2	4.8	289	4	Sequence 17, Appl
27	34.2	4.8	289	4	Sequence 17, Appl

28	34.2	4.8	1635	3	US-09-234-332-4	Sequence 4, Appl
29	34.2	4.8	5433	3	US-08-929-329-1	Sequence 1, Appl
30	34.2	4.8	20303	1	US-08-370-975B-6	Sequence 6, Appl
31	34.2	4.8	26764	1	US-08-370-975B-1	Sequence 1, Appl
32	34	4.7	1431	4	US-09-054-782-1	Sequence 1, Appl
33	34	4.7	1431	4	5466783-1	Patent No. 5466783
34	33.8	4.7	295	4	US-09-018-584A-8	Sequence 8, Appl
35	33.8	4.7	1209	4	US-09-105-537-21	Sequence 21, Appl
36	33.8	4.7	1798	2	US-08-557-128-12	Sequence 12, Appl
37	33.8	4.7	13613	4	US-09-105-537-3	Sequence 3, Appl
38	33.8	4.7	38506	3	US-09-320-878-19	Sequence 19, Appl
39	33.6	4.7	1065	1	US-08-145-006C-11	Sequence 11, Appl
40	33.6	4.6	291	4	US-09-329-796-1	Sequence 107, Appl
41	33.4	4.6	7208	3	US-09-166-186-107	Sequence 107, Appl
42	33.4	4.6	7208	3	US-09-313-932-107	Sequence 107, Appl
43	33.2	4.6	1065	5	US-08-854-764-1	Sequence 1, Appl
44	33.2	4.6	1065	5	PCRT-US95-09377-1	Sequence 1, Appl
45	33.2	4.6	1600	4	US-09-434-288-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-f1s
US-08-232-463-14

Query Match	6.1%	Score 44:	DB 1:	Length 7218;
Best Local Similarity	2.6%	Pred. No. 0.0055;		
Matches	8:	Conservative 180:	Mismatches 120:	Indels 0:

LOCATION: join(3..419, 421..2858)

S-08-232-463-14

FEATURE:	
NAME/KEY:	CDS


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; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: all n positions
; OTHER INFORMATION: n-a, c, g, or t
US-09-268-992-7

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Query Match          5.2%; Score 37.4; DB 4; Length 72604;
Best Local Similarity 58.6%; Pred. No. 1.1;
Matches 65; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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QY 539 tgccttccttcagtcacatcccatgtagtcttcctgctcctcgt 589
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 45295 TCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 45245
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RESULT 7
US-09-007-005-1/c
; Sequence 1, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/35003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 123
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-007-005-1

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Query Match          5.2%; Score 37.2; DB 4; Length 123;
Best Local Similarity 39.1%; Pred. No. 0.091;
Matches 36; Conservative 29; Mismatches 27; Indels 0; Gaps 0;

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```

QY 498 ttcaattgtttgtttcttcgccttccttccttccttccttccttcgta 557
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DB 115 TTTTCTTTTCTTTTCTTTGTYTCYAGGYTCYTCYTCYTCYTCYTCYTCY 56
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 558 ctcccatgtagtattcttcgttcgttcctcgtcgt 589
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 55 YTYCYAGGYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCY 24
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RESULT 8
US-09-244-796-1/c
; Sequence 1, Application US/09244796
; Patent No. 6283444
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/35007
; CURRENT APPLICATION NUMBER: US/09/244,796
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 123
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-796-1

```

```

Query Match          5.2%; Score 37.2; DB 4; Length 123;
Best Local Similarity 39.1%; Pred. No. 0.091;
Matches 36; Conservative 29; Mismatches 27; Indels 0; Gaps 0;

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DB 115 TTTTCTTTTCTTTTCTTTGTYTCYAGGYTCYTCYTCYTCYTCYTCYTCY 56
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 558 ctcccatgtagtattcttcgttcgttcctcgtcgt 589
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DB 55 YTYCYAGGYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCYTCY 24
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RESULT 9
US-09-339-964-1
; Sequence 1, Application US/09339964
; Patent No. 6025198
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
; FILE REFERENCE: RTS-0065
; CURRENT APPLICATION NUMBER: US/09/339,964
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 4743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(3988)
US-09-339-964-1

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CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,251
FILING DATE: No. 5883081 yet assigned
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,441
FILING DATE: 26-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 02307E-056410US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3168
OTHER INFORMATION: /label=pol
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US-08-659-251-14

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QY 495 tggttcaattgtttgtttctgcacctctctctctctctctctctctct 554
DB 248 CTGTACACCTCTGTATGATGATTCATTTTCTGCTCTTCTCTCTCTCTCT 189
QY 555 gcaaccacatgttatttctgtctgtctcctcgtcgtggttggtgactcgtccacc 614
DB 188 ACTTCTCTAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129
QY 615 gcaac 618
DB 128 GGAC 125

RESULT 13
US-09-256-490-14/c
Sequence 14, Application US/09256490
Patent No. 6235881
GENERAL INFORMATION:
APPLICANT: Kraus, Guenter
APPLICANT: Wong-Staal, Florsie
APPLICANT: Talbot, Randy
APPLICANT: Poeschia, Eric
TITLE OF INVENTION: Isolation of No. 6235881el HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,490
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,251
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 02307E-056410US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3168
OTHER INFORMATION: /label=pol
OTHER INFORMATION: /note="HIV-2KR subsequence encoding
US-09-256-490-14

Query Match 4.9%; Score 35.2; DB 4; Length 3168;
Best Local Similarity 49.5%; Pred. No. 1.3;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
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DB 308 GCAAAATCCCTGCGCCCTTTGTGTGCTCTCTCTTTCGAGGTGAGTAAGTCC 249
QY 495 tggttcaattgtttgtttctgcacctctctctctctctctctctctct 554
DB 248 CTGTACACCTCTGTATGATGATTCATTTTCTGCTCTTCTCTCTCTCTCT 189
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QY 615 gcaac 618
DB 128 GGAC 125

RESULT 14
PCT-US96-11445-14/c
Sequence 14, Application PC/TUS9611445
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruses
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Robins, Berlinger & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS


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1: APPLICATION NUMBER: US/08/659,251
2: FILING DATE: No. 5883081 yet assigned
3: CLASSIFICATION: 514
4: PRIOR APPLICATION DATA:
5: APPLICATION NUMBER: US 60/001,441
6: FILING DATE: 26-JUL-1995
7: ATTORNEY/AGENT INFORMATION:
8: NAME: Garrett-Wackowski, Eugenia
9: REGISTRATION NUMBER: 37,330
10: REFERENCE/DOCKET NUMBER: 02307E-056410US
11: TELECOMMUNICATION INFORMATION:
12: TELEPHONE: (415) 576-0200
13: TELEFAX: (415) 576-0300
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15: SEQUENCE CHARACTERISTICS:
16: LENGTH: 10163 base pairs
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18: STRANDEDNESS: single
19: TOPOLOGY: linear
20: MOLECULE TYPE: DNA (genomic)
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:31:48 ; Search time 13836.9 Seconds
(without alignments)
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Title: US-09-834-291-2

Perfect score: 1 gatccgcctgagcagcgcg95.....tggtcaatcaagagacgtg 720

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Searched: 21979536 seqs, 10817449327 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	716.8	99.6	45121	US-09-997-722-10	Sequence 10, Appl1
3	713	99.0	3212	US-09-834-291-1	Sequence 1, Appl1
4	611.8	85.0	2380	US-09-834-291-3	Sequence 4, Appl1
5	611.8	85.0	287	US-09-834-291-4	Sequence 3705, Appl1
6	296.8	41.2	467	US-60-172-360-3705	Sequence 32, Appl1
7	262.8	36.5	266	US-09-834-291-32	Sequence 818, Appl1
8	203.4	28.2	419	US-09-489-036-818	Sequence 818, Appl1
9	203.4	28.2	419	US-09-489-036-818	Sequence 818, Appl1
10	203.4	28.2	419	US-09-489-036-818	Sequence 818, Appl1
11	190.2	26.4	466	US-09-817-500-2214	Sequence 2214, Appl1
12	190.2	26.4	466	US-09-817-500-2214	Sequence 2214, Appl1
13	188.4	25.9	352	US-09-522-303-847	Sequence 847, Appl1
14	186.4	25.9	352	US-09-522-303-847	Sequence 847, Appl1
15	186.4	25.9	352	US-09-522-303-847	Sequence 847, Appl1
16	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
17	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
18	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
19	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
20	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
21	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
22	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
23	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
24	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
25	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
26	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
27	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
28	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
29	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
30	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
31	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
32	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
33	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
34	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
35	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
36	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
37	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
38	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
39	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
40	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
41	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
42	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1
43	182.6	25.4	473	US-09-234-611-3879	Sequence 3879, Appl1

Case	Year	Age	Gender	Marital Status	Occupation	Income	Assets	Liabilities	Net Worth	Debt-to-Income Ratio	Financial Health Score
C 32	1992	23.1	404	17	US-09-362-510A-3927	Sequence 3927, A					
C 33	1992	23.1	404	17	US-09-362-510A-3927	Sequence 3927, A					
C 34	1992	23.1	404	17	US-09-362-510A-3927	Sequence 3927, A					
C 35	1992	23.0	1655	56	US-60-172-373-10224	Sequence 10224, A					
C 36	1992	22.6	495	25	US-09-652-911-1924	Sequence 4924, A					
C 37	1992	22.1	318	25	US-09-652-127-2780	Sequence 2780, A					
C 38	1992	22.0	1732	25	US-09-644-667-7725	Sequence 7725, A					
C 39	1992	22.0	1732	25	US-09-652-911-10283	Sequence 10283, A					
C 40	1992	20.3	324	17	US-09-396-087-4122	Sequence 4122, A					
C 41	1992	15.2	2165	26	US-09-665-615B-94	Sequence 94, A					
C 42	1992	15.2	2165	31	US-09-802-669-94	Sequence 94, A					
C 43	1992	11.8	355	18	US-09-431-517-12091	Sequence 12091, A					
C 44	1992	11.8	355	18	US-09-431-517-12154	Sequence 12154, A					
C 45	1992	11.8	371	18	US-09-489-036-24950	Sequence 24950, A					

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Query Match	100.0%;	Score 720;	DB 32;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 2.4e-152;		
Matches 720;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 gatccgcgctgggacagcgcgagctcgcgcgtccctcggagaaccaatgcgtcccaagt 60
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Db 1 gattccgcctgggacagcgcgagctcgcgcgtccctcggagaaccaatgcgtcccaagt 60
| | | | |
QY 61 ggagtgaggcgtctgggggcccagacaagaattgaagcggaaagtcctgggaagctttaagttcgc 120
| | | | |
Db 61 ggagtgaggcgtctgggggcccagacaagaattgaagaagcggaaagtcctgggaagctttaagttcgc 120
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QY 121 tggagggggaccgcccggtctggagaagagagcggaaactccctgggacagccccctggacaagcccaa 180
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Db 121 tggagggggaccgcccggtctggagaagagagcggaaactccctgggacagccccctggacaagcccaa 180
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QY 181 gccaaaagctccgcgtctcgcgcgcggtctgggttggatctgcgcgcgccccgcggggcgggggagga 240
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Db 181 gccaaaagctccgcgtctcgcgcgcggtctgggttggatctgcgcgcgccccgcggggcgggggagga 240
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QY 241 gagcctaagaccttcacagaacaacatatgtctcaattcttcgcagttctcagaagctlagaaaa 300
| | | | |
Db 241 gagcctaagaccttcacagaacaacatatgtctcaattcttcgcagttctcagaagctlagaaaa 300
| | | | |
QY 301 taagtacagcacccggaagcagtggttaagcccggaagcgctcggagaacagcgaccctttctt 360
| | | | |
Db 301 taagtacagcacccggaagcagtggttaagcccggaagcgctcggagaacagcgaccctttctt 360
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QY 361 ctcgaaaagatcatatagggcgtagaatgaagcttcggggcgctgtttacccgttttttatc 420
| | | | |

Db	361	ctcgaaaaagtataatgaggggctgaatgagctctctggagcgctgtttaacgtttttatc	420
QY	421	gtccacagaagaaggaaatgcctgtgtccctccgggaattctctcttaagaactgta	480
Db	421	gtccacagaagaaggaaactgcctgtgtccctccgggaattctctcttaagaactgta	480
QY	481	agtcgctgcctgagatggtttcaattgtttgtttcttcgcctctctctctctcttg	540
Db	481	agtcgctgcctgagatggtttcaattgtttgtttcttcgcctctctctctctcttg	540
QY	541	cccttcttaagcttgcatcccaatgagatcttgccttggtcttcctgcgtgggttggtg	600
Db	541	cccttcttaagcttgcatcccaatgagatcttgccttggtcttcctgcgtgggttggtg	600
QY	601	tactcgtctccacgcacagaaaccggcgctatatttgcacagaagaacttggcagcct	660
Db	601	tactcgtctccacgcacagaaaccggcgctatatttgcacagaagaacttggcagcct	660
QY	661	gtttgaaagaatccctgcctcagaagaatgcagcgttgaagtgtgtaacaaagaacgtg	720
Db	661	gtttgaaagaatccctgcctcagaagaatgcagcgttgaagtgtgtaacaaagaacgtg	720

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RESULT 2
US-09-997-722-10
: Sequence 10, Application US/09997722
: GENERAL INFORMATION:
: APPLICANT: Morris, David
: APPLICANT: Engelhard, Eric
: TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
: FILE REFERENCE: A-71171/RMS/DCF
: CURRENT APPLICATION NUMBER: US/09/997,722
: CURRENT FILING DATE: 2001-11-30
: PRIOR APPLICATION NUMBER: US 09/747,377
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US 09/798,586
: PRIOR FILING DATE: 2001-03-02
: NUMBER OF SEQ ID NOS: 301
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 10
: LENGTH: 45121
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-997-722-10

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Query Match	99.6%;	Score 716.8;	DB 36;	Length 45121;
Best Local Similarity	99.7%;	Pred. No. 3.2e-151;		
Matches 718; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

[illegible]

QY 346 cggacacattctcttcgaaaaagtatatgaggcgtaagctcttgagctgt 405
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Db 2006 cggacacattctcttcgaaaaagtatatgaggcgtaagctcttgagctgt 2065
QY 406 ttacgctttttatgttcacacagaaaagaaactgctgtctccctccggaaattct 465
Db 2066 ttacgctttttatgttcacacagaaaagaaactgctgtctccctccggaaattct 2125
QY 466 ctcttaagacgttaagtcgctgctgagtggttcatctttgtttttctgcctt 525
Db 2126 ctcttaagacgttaagtcgctgctgagtggttcatctttgtttttctgcctt 2185
QY 526 ctcttctctcttttgcccttctcttagcttgacaccccaatggttctgctgtctcc 585
Db 2186 ctcttctctcttttgcccttctcttagcttgacaccccaatggttctgctgtctcc 2245
QY 586 tgcctggggttggtgtgactcgttcccaacgacagaaaccgagcctattatggccaag 645
Db 2246 tgcctggggttggtgtgactcgttcccaacgacagaaaccgagcctattatggccaag 2305
QY 646 aaacttgagcagcgtgttttgaagaagtcctcgcgtcagaagaatgcagcttcagatgct 705
Db 2306 aaacttgagcagcgtgttttgaagaagtcctcgcgtcagaagaatgcagcttcagatgct 2365
QY 706 aatcaagaagacgtg 720
Db 2366 aatcaagaagacgtg 2380

RESULT 5

US-09-834-291-4
; Sequence 4, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834, 291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4

Query Match 85.0%; Score 611.8; DB 32; Length 2827;
Best Local Similarity 99.7%; Pred. No. 9.2e-128;
Matches 613; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 106 aagcttagagtgctgtagaggggagcccggttgtagagagagagcgaaactccctgacaa 165
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Db 2213 aagcttagagtgctgtagaggggagcccggttgtagagagagagcgaaactccctgacaa 2272
QY 166 gccctgcaaacgcaagcgaaggtccgctcgcgagcggtgtagagtcgagcgccccc 225
|||||
Db 2273 gccctgcaaacgcaagcgaaggtccgctcgcgagcggtgtagagtcgagcgccccc 2332
QY 226 gcgggggcgggagagagcctacagccttcagaaacacatattgctcattttctggcagtt 285
2333 gcgggggcgggagagagcctacagccttcagaaacacatattgctcattttctggcagtt 2392
QY 286 ctgagagctaggaataagtagacacggaacagtcgtttagcgcgagaggtctcgaaaga 345
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Db 2393 ctgagagctaggaataagtagacacggaacagtcgtttagcgcgagaggtctcgaaaga 2452

QY 346 cggacacattctcttcgaaaaagtatatgaggcgtaagctcttgagctgt 405
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QY 406 ttacgctttttatgttcacacagaaaagaaactgctgtctccctccggaaattct 465
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Db 2813 aatcaagaagacgtg 2827

RESULT 6

US-60-172-360-3705/C
; Sequence 3705, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172, 360
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 3705
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 038693.2C
US-60-172-360-3705

Query Match 41.2%; Score 296.8; DB 56; Length 467;
Best Local Similarity 99.3%; Pred. No. 9.1e-57;
Matches 298; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 421 gtacacagaaaagaaactgctgtctccctccggaaattctctttaagactgta 480
Db 467 gtacacagaaaagaaactgctgtctccctccggaaattctctttaagactgta 408
QY 481 agtcgctcgtgagtggttcaattgtttgtttttcttcgcttctctctttt 540
Db 407 agtcgctcgtgagtggttcaattgtttgtttttcttcgcttctctctttt 348
QY 541 cctttcttagcttgacatccacatgagtgatcttcgtctgtctcctcgtggtgtg 600
Db 347 cctttcttagcttgacatccacatgagtgatcttcgtctgtctcctcgtggtgtg 288
QY 601 taactgtccacacagaaacccgagcctattatgtgcgaagaacttgagacgt 660
Db 287 taactgttttccacacagaaacccgagcctattatgtgcgaagaacttgagacgt 228


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; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: US 09/235,076
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: US 09/234,611
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: US 09/240,371
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: US 09/277,227
; EARLIER FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 09/271,490
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 09/293,972
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 09/274,861
; EARLIER FILING DATE: 1999-03-23
; EARLIER APPLICATION NUMBER: US 60/125,453
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/126,605
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 09/306,350
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/399,720
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: US 09/404,284
; EARLIER FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 10451
; SOFTWARE: PL_CT_genes Version 1.0
; SEQ ID NO 3315
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (465)...(578)
; OTHER INFORMATION: similar to g1178067 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-471-275-3315

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Query Match      28.2%; Score 203.4; DB 18; Length 575;
Best Local Similarity 99.5%; Pred. No. 1.2e-35;
Matches 204; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatccgcgttgaggagcgggagcagctccgcgcctctcgagagaccactgcgtccagct 60
   |||
Db 313 GACCCCGCTGGGAGGAGGCGGAGCTCCGGCGCTCTCGAGACCTGCGCTCCAGCTT 254
   |||
QY 61 gaggttgagcgttgaggagcgggagcaggaattgaagcggaagctctggaagctttaggtcgc 120
   |||
Db 253 GAGGTGGCGGTGGGGGCGGACAGATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTGC 194
   |||
QY 121 tggaggaggagcccggttggagagagagcgaactcttgacaagccctacaagccaa 180
   |||
Db 193 TCGAGGGGAGCCCGGCTTGAGAGAGAGGAGGAGGAACTCTTGACAAAGCCCTGACAAAGCAA 134
   |||
QY 181 gccaaagtcgcgtccggagcgaggt 205
   |||
Db 133 GCCAAGGTCCTCGGCGGGGT 109

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```

RESULT 11
US-09-333-909-2214
; Sequence 2214, Application US/09333909
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: MLN98-29PM
; CURRENT APPLICATION NUMBER: US/09/333,909
; CURRENT FILING DATE: 1999-06-16

```

```

; EARLIER APPLICATION NUMBER: 60/089,519
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/135,628
; EARLIER FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 2409
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2214
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(466)
; OTHER INFORMATION: n = A,T,C or G
US-09-333-909-2214

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Query Match      26.4%; Score 190.2; DB 17; Length 466;
Best Local Similarity 87.7%; Pred. No. 1.1e-32;
Matches 207; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 288 cagacgtaggaaataagtcagcaccgaagcagtggttaagccgagggctcgaaagacg 347
   |||
Db 15 cggacgtaggaaataagtcagcaccgaagcagtggttaagccgagggctcgaaagacg 74
   |||
QY 348 gcaacgtttcttctcgaaaaagtataatgaggcgtgaatgactcttgagagcttggtt 407
   |||
Db 75 gcaacgtttcttctcgaaaaagtataatgaggcgtgaatgactcttgagagcttggtt 134
   |||
QY 408 accgttttcttctcgaaaaagtataatgaggcgtgaatgactcttgagagcttggtt 467
   |||
Db 135 accgttttcttctcgaaaaagtataatgaggcgtgaatgactcttgagagcttggtt 194
   |||
QY 468 ctttaagactgtatgcgtgcctgagtggttcaattgtttgtttttctgcc 523
   |||
Db 195 ctttaagactgtatgcgtgcctgagtggttcaattgtttgtttttctgcc 250
   |||

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RESULT 12
US-09-817-500-2214
; Sequence 2214, Application US/09817500
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600.1029-002
; CURRENT APPLICATION NUMBER: US/09/817,500
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/089,519
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/135,628
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: US 09/333,909
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 2409
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2214
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(466)
; OTHER INFORMATION: n = A,T,C or G
US-09-817-500-2214

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Query Match      26.4%; Score 190.2; DB 31; Length 466;
Best Local Similarity 87.7%; Pred. No. 1.1e-32;
Matches 207; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 288 cagacgtaggaaataagtcagcaccgaagcagtggtttagccgagggctcgaaagacg 347

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Mon Sep 9 09:30:27 2002

us-09-834-291-2.rmp

Page 8

Search completed: September 7, 2002, 22:32:03
Job time: 43817 sec

Db	10794	taagtgcagcccgcaagcagtggtttaagccggagagcttcgaaagaagcgccttctctt	10855
QY	361	ctcggaaaaagttatagggggcctgtaatgagctctcvgagagcttgtttaccgtttttatt	420
Db	10854	ctcgaaaaagttatatacgggggctgtaataagctctctcgaagagcttgtttaccgtttttatt	10911
QY	421	gtcacacagaaaaagagaactcgtctctcccccctccgggaattcctctcttaagactgtg	480
Db	10914	gtcacacagaaaaagagaactcgtctctcccccctccgggaattcctctcttaagactgtg	10973
QY	481	atctcgtcgtcctagtagtggttcaatttggttttcttcgcctctctctctctcttg	540
Db	10974	atctcgtcgtcctagtagtggttcaatttggttttcttcgcctctctctctctcttg	11033
QY	541	ccctctctctagttgcacctcccatgtagttctcgtctgctctcctcgtcgggttggtg	600
Db	11034	ccctctctctagttgcacctcccatgtagttctcgtctgctctcctcgtcgggttggtg	11093
QY	601	tactcgttcccaacccgacagaaccccgcgcgctattattggtcccaagaactatgacagcct	660
Db	11094	tactcgttcccaacccgacagaaccccgcgcgctattattggtcccaagaactatgacagcct	11153
QY	661	gttttgaagaagttccctcgtctcagaatgtccagacttgacagtgcgtcaataccaagaagctg	720
Db	11154	gttttgaagaagttccctcgtctcagaatgtccagacttgacagtgcgtcaataccaagaagctg	11213

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RESULT      2
US-10-222-927-123/c
; Sequence 123, Application US/10222927
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM006CIN
; CURRENT APPLICATION NUMBER: US/10/222,927
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/758,465
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 1276
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-222-927-123

```

[illegible]

```
RESULT 3
US-10-198-846-8585
; Sequence 8385, Application US/10198846
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steilmann, Kathleen
```

```

1  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
2  TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
3  TITLE OF INVENTION: THERAPY OF BREAST CANCER
4  FILE REFERENCE: MRI-049
5  CURRENT APPLICATION NUMBER: US/10/198, 846
6  CURRENT FILING DATE: 2002-07-18
7  PRIOR APPLICATION NUMBER: 60/306,220
8  PRIOR FILING DATE: 2001-07-18
9  NUMBER OF SEQ. ID NOS: 14084
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ. ID NO 6585
12 LENGTH: 931
13 TYPE: DNA
14 ORGANISM: Homo sapiens
15 FEATURE:
16 NAME/KEY: misc_feature
17 LOCATION: 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21
18 LOCATION: 22, 24, 27, 28, 36, 66, 68, 78, 86, 87, 115, 117, 133, 142
19 LOCATION: 143, 157, 158, 162, 165, 173, 176, 177, 183, 184, 186, 188
20 LOCATION: 200, 201, 203, 206, 207, 213, 214, 215, 217, 221, 222
21 OTHER INFORMATION: n = A,T,C or G
22 FEATURE:
23 NAME/KEY: misc_feature
24 LOCATION: 229, 231, 232, 256, 294, 295, 299, 309, 310, 317, 331, 334
25 LOCATION: 339, 344, 357, 360, 361, 363, 366, 369, 380, 387, 397, 407
26 LOCATION: 412, 418, 424, 426, 428, 433, 437, 441, 444, 456, 459, 460
27 LOCATION: 462, 463, 470, 471, 472, 478, 503, 506, 520, 528, 538
28 OTHER INFORMATION: n = A,T,C or G
29 FEATURE:
30 NAME/KEY: misc_feature
31 LOCATION: 541, 542, 544, 550, 554, 555, 557, 561, 569, 580, 595, 597
32 LOCATION: 607, 629, 638, 658, 660, 663, 666, 675, 701, 703, 710, 712,
33 LOCATION: 718, 724, 726, 728, 732, 735, 746, 749, 754, 759, 761, 764,
34 LOCATION: 770, 773, 779, 780, 792, 800, 801, 822, 824, 825, 826
35 OTHER INFORMATION: n = A,T,C or G
36 FEATURE:
37 NAME/KEY: misc_feature
38 LOCATION: 832, 833, 843, 845, 854, 868, 872, 874, 885, 892, 897, 900,
39 LOCATION: 909, 929, 930
40 OTHER INFORMATION: n = A,T,C or G
41 US-10-198-846-8585

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[illegible]

RESULT 4
US-10-098-754-7588/c
Sequence 7588, Application US/10098754
GENERAL INFORMATION:
APPLICANT: Harrington, John J.
APPLICANT: Jackson, P. David
APPLICANT: Sherf, Bruce A.
APPLICANT: Cain, Scott
APPLICANT: Rindlett, Stephen E.

PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 325093
LENGTH: 787
TYPE: DNA
ORGANISM: Human
US-10-027-632-325093

Query Match
Best Local Similarity 55.6%; Score 40; DB 7; Length 787;
Matches 70; Conservative 3; Mismatches 53; Indels 0; Gaps 0;

QY 424 acacagaaaggaactgctgtccctccggaattcctcttaagaactgaagt 483
DB 556 AAAAAAAAAAACTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 497
QY 484 cgcctgcctgagtgcttcttcttcttcttcttcttcttcttcttcttcc 543
DB 496 TCTTCT 437
QY 544 tctctct 549
DB 436 TTTCTT 431

RESULT 11
US-10-103-313-632
Sequence 632, Application US/10103313
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 633
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 632
LENGTH: 6573
TYPE: DNA
ORGANISM: Homo sapiens
US-10-103-313-632

Query Match
Best Local Similarity 5.6%; Score 40; DB 7; Length 6573;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 358 ttctcgaaagtaataatgagctgaatgagctctggaagctgttaccgttttt 417
DB 3892 tctatcgagataatcatgtgttttgcattgtcttgaatgagatlaagctt 3951
QY 418 attgcaacagaaagaaactgctgtctccctccggaattctcttcttaagact 477
DB 3952 attgattgcatatctcgaacagccttgcatctccagagatgaagcaactgcatc 4011
QY 478 gtaagtcgctgagtgcttcttcttcttcttcttcttcttcttcttctt 537
DB 4012 gtttctgagatgctgcgcatcatttccagattttattgagattttgcatcaa 4071

QY 538 ttgaccttcttagctgacatcccatgtgattctctctctctctctgaggttg 597
DB 4072 tgtcatcagcatatgctcctgaatttcttcttcttcttcttcttcttcttct 4131

RESULT 12
US-10-125-540-561/c
Sequence 561, Application US/10125540
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ214C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 561
LENGTH: 6573
TYPE: DNA
ORGANISM: Homo sapiens
US-10-125-540-561

Query Match
Best Local Similarity 47.9%; Score 40; DB 7; Length 6573;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 358 ttctcgaaagtaataatgagctgaatgagctctggaagctgttaccgttttt 417
DB 2682 tctatcgagataatcatgtgttttgcattgtcttgaatgagatlaagctt 2623
QY 418 attgcaacagaaagaaactgctgtctccctccggaattctcttcttaagact 477
DB 2622 ATTGATTGATGATGCTGAACCAAGCTTGATTCCTAGGAGTAAGCACTTATCAT 2563
QY 478 gtaagtcgctgagtgcttcttcttcttcttcttcttcttcttcttctt 537
DB 2562 GTTTTTCGATGCTGCTGATTCATTTTGCAGATTTTATGAGATTTTGCATCAA 2503
QY 538 ttgaccttcttagctgacatcccatgtgattctctctctctctctgaggttg 597
DB 2502 TGTTCATCAGGATATTGCGCTGAATTTTCATTTTGTGATGCTGCGAGGTTTG 2443

RESULT 13
US-10-158-057-375
Sequence 375, Application US/10158057
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ205C1
CURRENT APPLICATION NUMBER: US/10/158,057
CURRENT FILING DATE: 2002-06-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 375
LENGTH: 6573
TYPE: DNA
ORGANISM: Homo sapiens
US-10-158-057-375

Query Match
Best Local Similarity 47.9%; Score 40; DB 7; Length 6573;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 358 ttctcgaaagtaataatgagctgaatgagctctggaagctgttaccgttttt 417
DB 3892 tctatcgagataatcatgtgttttgcattgtcttgaatgagatlaagctt 3951

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:28 ; Search time 8462.63 Seconds
(without alignments)
1148.320 Million cell updates/sec

Title: US-09-834-291-2
720

Perfect score: 1 gatccgcctggcagcagcggg.....tgctatcaagaagacgtg 720

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: em_hic:*
9: gb_estl:*
10: gb_estl:*
11: gb_hic:*
12: gb_hic:*
13: em_gss_hum:*
14: em_gss_hum:*
15: em_gss_hum:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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C 2	298.4	41.4	603	9	AA058563
C 3	294.4	40.9	577	9	AA058563
C 4	286.4	39.8	442	9	AA011028
C 5	285.4	39.6	447	9	AA047220
C 6	276.4	38.4	467	9	AA020992
C 7	270	37.5	376	10	H84298
C 8	259	36.0	398	10	H86126
C 9	254.4	35.3	297	9	AA018441
C 10	253.6	35.2	381	10	H86544
C 11	197	27.4	419	10	R85827
C 12	190	26.4	696	9	AL540709
C 13	185.2	25.7	696	9	AV15411
C 14	181.8	25.2	828	10	BI838027
C 15	177	24.6	506	10	BG659530
C 16	148.4	20.6	599	10	BF569266

C 18	142.2	19.7	1140	10	BG121070	BG121070
C 19	140	19.4	617	9	AV695647	AV695647
C 20	124	17.2	359	9	AV692383	AV692383
C 21	96	13.3	285	10	BM090262	BM090262
C 22	63.4	8.8	800	10	BI463384	BI463384
C 23	62.4	8.7	291	9	AA383161	AA383161
C 24	52	7.2	1101	12	CNS00LJC	AL068290
C 25	51	7.1	844	12	CNS0052P	AL056652
C 26	49.6	6.9	912	12	CNS006N3	AL065775
C 27	49.4	6.9	821	10	BI956860	BI956860
C 28	47.4	6.6	925	12	CNS0091P	AL053013
C 29	47	6.5	1101	12	CNS00BOM	AL056623
C 30	46.8	6.5	931	12	CNS005QH	AL061369
C 31	46.8	6.5	1035	9	AL578906	AL578906
C 32	46.4	6.4	910	12	CNS006ON	AL063829
C 33	46.2	6.4	854	10	BI950608	BI950608
C 34	46	6.4	272	9	AW185154	AW185154
C 35	45.8	6.4	696	10	BM58974	BM58974
C 36	45.8	6.4	1326	9	AW731214	AW731214
C 37	45.6	6.3	474	10	BG520290	BG520290
C 38	45.6	6.3	985	12	CNS02R29	AL1210042
C 39	45.6	6.3	1101	12	CNS00GFB	AL072375
C 40	45.2	6.3	802	12	CNS02R43	AL210108
C 41	45.2	6.3	851	9	AL514003	AL514003
C 42	44.8	6.2	631	9	AL566993	AL566993
C 43	44.8	6.2	724	12	AG058793	AG058793
C 44	44.8	6.2	1050	10	BF248086	BF248086
C 45	44.6	6.2	1064	12	CNS016P9	AL107031

ALIGNMENTS

RESULT 1
BI763679/c 793 bp mRNA linear EST 25-SEP-2001
603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
LOCUS
DEFINITION
mRNA sequence.

ACCESSION
BI763679
VERSION
BI763679.1 GI:15755257
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 793)
NIH-MGC http://mgs.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLM11474 row: e column: 17
High quality sequence stop: 786.
Location/Qualifiers
1..793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5189752"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is

FEATURES

source

[illegible]

Db	241	GTTTGAAGAGTCCTCCCTGCTCAGAAATGCCAGCTTGCGCATATGGCTAATACNAGAGACGCG	300
RESULT	4		
AA011028			442 bp mRNA linear EST 29-NOV-1996
LOCUS			
DEFINITION	AA011028		z634d02.s1 Soares retina N2b4HR Homo sapiens cDNA clone
ACCESSION	AA011028		IMAGE:360867 3', mRNA sequence.
VERSION	AA011028		
KEYWORDS	AA011028.1	GI:1472055	
SOURCE			EST.
ORGANISM			human.
REFERENCE			Homo sapiens
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 442)
TITLE			Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman , M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Ritkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston , R., Williamson,A., Wohlmann,P. and Wilson,R. The Mashu-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 844 Std Error: 0.00 Seq primer: mob.REGA+FR High quality sequence stop: 372.
JOURNAL			Location/Qualifiers
COMMENT			1..442
FEATURES			/organism="Homo sapiens"
source			/db_xref="GBD:1277412"
			/db_xref="taxon:9606"
			/clone="IMAGE:360867"
			/clone_1lb="Soares retina N2b4HR"
			/sex="male"
			/tissue_type="retina"
			/dev_stage="55 year Old"
			/lab_host="DH10B (ampicillin resistant)"
			/note="Organ: eye; Vector: pTV73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TCATTGCATCTGAAGTAGGAGCGGCCGCCGCTTTTTTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTV73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Felima Bonaldo."
BASE COUNT	92 a	107 c	103 g 138 t 2 others
ORIGIN			
Query Match			39.8%; Score 286.4; DB 9; Length 442;
Best Local Similarity			99.0%; Pred. No. 3.5e-43;
Matches 298; Conservative			0; Mismatches 2; Indels 1; Gaps 1.
Oy	421	gtcacacagaaagggaactccttgctgccttcgscggagaattctctctaagaact-gt	479
Db	1	GTGNCAAGAAAAAACCTGCTGTCTCCCTTCGCCGGAATTCCTTAAGACNGT	60
Oy	480	aagtgcgcgcctgaatggtttcatlttgttttgtttcttgcacctctctctctctttt	539
Db	61	AAATGCGCTCCGACTGCTTTCATTTTGTGTTTTCGCCCCCTTCCTTCTCTTTT	120

QY	540	gaccccttcttaacttgcgaatcccaatgagtaattctcgtctgtatcctcgtcgtggtgtgtg	539
Db	121	gccccttcttcttaacttgcgaatcccaatgagtaattctcgtctgtatcctcgtcgtggtgtgtg	180
QY	600	gtaccgcgttcaccgcgcgaacagaacccggcgccatattatgtggccaagaaccttgaagcc	659
Db	181	gtactcgtttccaccgcgcgaacagaacccggcgccatattatgtggccaagaaccttgaagcc	240
QY	660	tgttttgaagaagtcacctgcgtcagaatltccagctltgcagatlggtcctaatcaagaagagct	719
Db	241	tgttttgaagaagtcacctgcgtcagaatltccagctltgcagatlggtcctaatcaagaagagagct	300
QY	720	g 720	
Db	301	G 301	

RESULT	5	547 bp	mrna	linear	EST
AA047220					02-FEB-1997
LOCUS					
DEFINITION					
ACCESSION	AA047220	z49gell.1	Soares retina	Nb4hr	Homo sapiens cDNA clone
VERSION	AA047220	IMAGE:380300	3', mRNA sequence.		
KEYWORDS	AA047220.1	GI:1525120			
SOURCE	EST.				
ORGANISM	human.				
	Homo sapiens				

REFERENCE
1 (bases 1 to 547)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, R., et al. 1992. *Endicarda*, Primates; Catarrhini; Homiidae; Homo.

Cunniffe, S., Dietrich, N., Dubugue, T., Favello, A., Gish, W., Hawkins
 M., Hultman, M., Kucata, T., Lacy, M., Le, N., Mardis, E., Moore
 B., Morris, M., Parsons, J., Pringle, C., Rikkin, L., Rohling, T.,
 Schellenberg, K., Soares, M.B., Tan, E., Thierly-Meg, J., Trevisan, S., E.,
 Underwood, K., Wohldmann, P., Waterson, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 970444/8
 Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 893 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 471.

source

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/organism="Homo sapiens"
/db_xref="GDB:1288557"
/db_xref="taxon:9606"
/clone="IMAGE:380300"
/clone_1ib="Soares retina N2b4HR"
/sex="male"
/tissue="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pRT73D (Pharmacia) with a
modified polylinker. Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5
TGTTCACATCTGCAATGTGGAGCGCGCCCTCTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(a)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento

```

BASE COUNT	Soares and M.Fatima Bonaldo, "
131 a	128 c
125 g	158 t
5 others	

Query Match	39.8%	Score 286.4;	DB 9;	Length 547;
Best Local Similarity	99.3%;	Pred. No. 3.4e-43;		
Matches 298;	Conservative	0;	Mismatches 1;	Indels 1;
				Gaps 1;

[illegible]

RESULT	6
LOCUS	AA057418
DEFINITION	AA057418 447 bp mRNA linear EST 18-SEP-1996
ACCESSION	Zf59n03.s1 Soares retina N2b4HR Homo sapiens CDNA clone
VERSION	AA057418
KEYWORDS	IMAGE:381269 3', mRNA sequence.
SOURCE	AA057418.1 GI:1550059
EST.	human.

ORGANISM	TITLE	JOURNAL	REFERENCE	AUTHORS
<i>Homo sapiens</i>				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
1 (bases 1 to 447)				
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman				
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,				
Rifkin, L., Rollfing, T., Soares, T., Tan, F., Treviskis, E., Waterston				
, R., Williamson, A., Woldmann, P. and Wilson, R.				
The WashU-Merck EST Project				
Unpublished (1995)				
Contact: Wilson RK				

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estevatson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 339.
Location/Qualifiers
1..447

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/organism="Homo sapiens"
/db_xref="GDB:1289532"
/db_xref="taxon:9606"
/clone="IMAGE:381269"
/clone_lib="Scares retina N2b4R"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT73D (Pharmacia) with a
modified polylinker: Ste1: Not I; Site2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'

```


TITLE 'R', Williamson, A., Wohldmann, P. and Wilson, R
JOURNAL The Washu-Merck ESR Project
COMMENT Unpublished (1995)
Contact: Wilson RK

.R., Williamson, A., Mohlmann, P. and Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 364
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 881 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 364

FEATURES

Source

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/organism="Homo sapiens"
/db_xref="GDB:3851329"
/db_xref="taxon:9606"
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/clone_1ib="Soares retina N2b5HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pT73D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - 01190(dT) primer (5
TGTTCACCACTCGAAGTCGAGCGGCCCGCTTTTCTTTTCTTTTCTT
3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaldo. "

```

Query Match	37.5%	Score 270	DB 10	Length 376
Best Local Similarity	100.0%	Pred. No. 3,7e-40		
Matches 270	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	1	ccttcgcggaaattctctcttttaagaactgaaatccgctgcctaaagtgttcattgttt	60	
QY	511	tgttttttcgcgcctctctctctctctcttttgcgccttttaagtgcactcccatgtagt	570	
Db	61	tgttttttcgcgcctctctctctctctcttttgcgccttttaagtgcactcccatgtagt	120	
QY	571	ttctgcttggatctcctctgctgggttggtagtactcgttcccaaccgacaagaaccggagc	630	
Db	121	tttgccttggatctcctctgctgggttggtagtactcgttcccaaccgacaagaaccggagc	180	
QY	631	cttatattgggcacaagaactgtagcagcctgttttgaagaagtcctcctgctcagaatgcc	690	
Db	181	cttatattgggcacaagaactgtagcagcctgttttgaagaagtcctcctgctcagaatgcc	240	
QY	691	agcttcgacagatgctcaatccaagaagactgtg	720	
Db	241	agcttcgacagatgctcaatccaagaagactgtg	270	

RESULT	9				
H86126					
LOCUS	H86126	398 bp	mRNA	linear	EST 21-NOV-1995
DEFINITION	y9594g8.s1	Soares retina	N2b5HR	Homo sapiens	CDNA clone

ACCESSION	H86126	Accession number
VERSION	H86126.1	Version number
KEYWORDS	EST.	Keywords
SOURCE	human.	Source
ORGANISM	Homo sapiens	Organism

REFERENCE
AUTHORS

Pachamelaia, Euterria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 398)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.

TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 378
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 925 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 378.

FEATURES

Source

BASE COUNT
ORIGIN

74 a 93 c 105 g 125 t 1 others

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/db_xref="taxon:9606"
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/clone_lib="Soares retina N25HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: eye; Vector: pTV73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5
tggtaccacatctgaagtcgacgcgcgcctttttttttttttttttttttt 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTV73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M. Fatima Bonaldo. "
```

Query Match	36.0%;	Score 259;	DB 10;	Length 398;
Best Local Similarity	99.6%;	Pred. No. 3.9e-38;		
Matches 270; Conservative	0;	Mismatches	0.	Totals 1.

[illegible]

Db		181	GGGCGCTATTATTTGCGCAAGAACTTGACAGCCCTTGTGAAGAAGTCCTCCTGCCTCACAGA	240
Oy	686	atgccagcttgcga-gattggtcaataccaagaq	715	
Db	241	ATGCCAAGCTTGCGAGATGCGTAATAACAAGG	271	
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DEFINITION	250608.s1 Soares retina N2B4HR Homo sapiens CDNA clone			
ACCSSION	AAO18441			
VERSION	AAO18441.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. Haller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman , M., Hultman,M., Kucba,T., Le,M., Lennon,G., Maria,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Watson, .R., Williamson,A., Wohlmann,P. and Wilson,R. The WashU-Merck Est Project Unpublished (1995) Contact: Wilison RK Washington University School of Medicine 444 Forest Park Parkway, Box B501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@atson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (image.lnl.gov) for further information. Seq primer: -40M13 fwd. from Amershams High quality sequence stop: 244. Location/Dualifiers			
TITLE	JOURNAL			
COMMENT				
FEATURES	source			
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	/db_xref="GeneDB:1279093"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:362390"			
	/clone_id="Soares retina N2B4HR"			
	/sex="male"			
	/issue_type="retina"			
	/dev_stage="55 year old"			
	/lab_host="DH10B (ampicillin resistant)"			
	/note="(Organ: eye; Vector: pRTV3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st tstrand cDNA was primed with a Not I - oligo(dT) primer [5'] TGTTACCAACTGAAAGTAGGAGCGGCGCGGTGTGTTTTTTTTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRTV3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the university of Toronto. Library constructed by Bento Soares and M.Paulna Bonaldo."			
BASE COUNT	59 A 78 C 62 G 98 T			
ORIGIN				
Query Match	35.3%; Score 254.4; DB 9;			
Best Local Similarity	99.6%; Pred.No.2.9e-37;			
Matches	255; Conservative			
	0; Mismatches			
	1; Indels			
	0; Gaps			
	0;			
Oy	423	cacacagaaaaggaaactgccttgttcctccotcggsgaatctctctttaagaagtgaag	482	
Db	1	CACACAGAAAAAGAACCTGCTGTCTCCCTTCGGGAAFTGCTCTTAAGACTGTAG	60	

OY	483	tgcgctcgtcgagtgagttatatttggtttctgtttcttcgccctccctcttcttccttgc	542
Db	61	TTCGCTCCCTGAGTGGGTTTCAATTTGTGTTTTGTTTTCTTTCGCCCTTCCTCCTTTCGCC	120
OY	543	ccttcctaagtcatccacatcgaatglatctctgtgtcctcctgtcgtagggttgtgtgta	602
Db	121	CCTTCTTAGTTCACACTCCCATCGTAATTTCGCTGTCCTGCTGGGCTTGGGTA	180
OY	603	cctcgtccaccgcgcacagaacccgcgccttatattgtgccaagaactctgagcaacctgt	662
Db	181	CTCGTTTCCCACCACAGAACC CGGCCTATTATTGCGCAMAAACTTGACAGCCCTGT	240
OY	663	tttgaaaagtcctcctcg	678
Db	241	TTTTGAAGAATCCCTCG	256
RESULT	11		
H86544			
LOCUS		381 bp	mRNA linear EST 21-NOV-1995
DEFINITION		IMAGE:223321 3', mRNA sequence.	
ACCESSION	H86544		
VERSION	H86544.1	GI:1068123	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 381) Haller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maria,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston ,R., Williamson,A., Wohlmann,P. and Wilson,R. The Wash-Merck EST Project Unpublished (1995)		
JOURNAL	Contact: Wilison RK		
COMMENT	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 361 Source: IMAGE Consortium, LNL. This clone is available royalty-free through LNL.; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 882 Std Error: 0.00 Seq primer: Promega -2lm13 High quality sequence stop: 361. Location/Qualifiers 1..381 Organism="Homo sapiens" /db_xref="GDB:385435" /db_xref="taxon:9606" /clone="IMAGE:223321" /clone_lib="Soares retina N2B5HR" /sex="male" /tissue_type="retina" /dev_stage="55 year old" /lab_host="DH10B (ampicillin resistant)" /note="Organ: eye; Vector: pTR73D (Pharmacia) with a modified polylinker; Site_1: Not I ; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACAATCTGAGTGGGAGCGCGCGCTGTGTTTTTTTTTTTTTTT 3'] , RT adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTR73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Falma Bonaldo."		

100

OY 419 ttgtcacacagaaagaaactgcttgctccctccgggaattctctcttaagactg 478
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 Db 121 TTGTACACACAGAAAGAACTGCTGTCTCCCTTCGCGGAATTCCTTAAGACTG 180
 OY 479 taagtcgctgacctgagtggttcaatttggtttcttctgccc 523
 |||||
 Db 181 TTCTTACGCTGTGTGCTAGATTATCGTCCAAAGTGTTAATGCC 225

Search completed: September 7, 2002, 14:51:33
 Job time: 16192 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:16 ; Search time 8462.63 Seconds
(without alignments)
31.898 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
Sequence: 1 agagatgcccaactgtttt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gD_est1:*
10: gD_est2:*
11: gD_hic:*
12: gD_gss:*
13: em_gss_hum:*
14: em_gss_iny:*
15: em_gss_pln:*
16: em_gss_vtc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	17.4	87.0	282	9	BB573416
2	17.4	87.0	475	10	BM420516
3	17.4	87.0	677	10	BC410123
4	17.4	87.0	735	9	BB630820
5	17.4	87.0	796	12	BB393256
6	17.4	85.0	627	9	AL575246
7	17.4	85.0	948	9	AL551725
8	16.8	84.0	200	12	AZ766513
9	16.8	84.0	291	9	AA400303
10	16.8	84.0	302	10	BF994308
11	16.8	84.0	314	10	BF994307
12	16.8	84.0	322	12	AZ719811
13	16.8	84.0	326	9	BB508020
14	16.8	84.0	365	10	D60325
15	16.8	84.0	377	9	AM879474
16	16.8	84.0	385	10	BF994425
17	16.8	84.0	394	12	AZ231468

18	16.8	84.0	411	12	A0173492	A017492 HS_3193_A
19	16.8	84.0	498	10	BG726816	BG726816 sae27c11
20	16.8	84.0	532	10	BM054898	BM054898 1e83907.y
21	16.8	84.0	535	9	AM704890	AM704890 sk40h01.y
22	16.8	84.0	546	12	A0992080	A0992080 nbe00080C
23	16.8	84.0	563	10	BF191086	BF191086 237803 MA
24	16.8	84.0	578	12	AZ909829	AZ909829 RPCT-24-2
25	16.8	84.0	667	12	AG037563	AG037563 Pan t10g1
26	16.8	84.0	678	10	BJ069294	BJ069294 Bt096294
27	16.8	84.0	783	12	AG094259	AG094259 Pan t10g1
28	16.8	84.0	809	12	A0850057	A0850057 nbe00114E
29	16.8	84.0	1021	12	CNS02180	CNS02180 Tetradon
30	16.8	84.0	1612	10	BF179654	BF179654 601806044
31	16.4	82.0	103	9	A1561272	A1561272 tq23905.x
32	16.4	82.0	270	9	BB195068	BB195068 Bt195068
33	16.4	82.0	339	9	BB224461	BB224461 BB224461
34	16.4	82.0	370	10	BG230189	BG230189 uv03912.x
35	16.4	82.0	443	9	A0023648	A0023648 A0023648
36	16.4	82.0	468	12	A0887814	A0887814 HS_5564_A
37	16.4	82.0	469	9	A1682696	A1682696 wc65805.x
38	16.4	82.0	480	9	AM643847	AM643847 cm34609.y
39	16.4	82.0	481	12	AZ583912	AZ583912 1M0388A12
40	16.4	82.0	496	12	AQ305214	AQ305214 HS_2019_A
41	16.4	82.0	525	12	AZ120201	AZ120201 RPCT-23-2
42	16.4	82.0	548	10	BE750959	BE750959 202641 MA
43	16.4	82.0	594	12	AQ249605	AQ249605 F10P24-T7
44	16.4	82.0	644	12	AZ336189	AZ336189 1M0066P17
45	16.4	82.0	649	9	BB645432	BB645432 BB645432

ALIGNMENTS

RESULT 1
BB573416 282 bp mRNA linear EST 30-NOV-2000
BB573416 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930501C15 5', mRNA sequence.

ACCESSION
BB573416
VERSION
BB573416.1
KEYWORDS
GI:11469960
SOURCE
house mouse.
ORGANISM
Mus musculus

REFERENCE
Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arahawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hirooka,T., Hirozane,T., Hodojima,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shigaawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,T., Toya,T., Watanishi,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Aizawa,K. et al. 2000)

TITLE
JOURNAL
COMMENT
unpublished (2000)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,M., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermolabile and thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Katsunari,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

Db 46 GAGATGCCCAACTGTTT 28

RESULT 4 735 bp mRNA linear EST 26-OCT-2001
LOCUS BB630820 RIKEN full-length enriched, 16 days neonate thymus Mus
DEFINITION Musculus CDNA clone A130029622 5', mRNA sequence.
ACCESSION BB630820
VERSION BB630820.1 GI:16467689
KEYWORDS EST.
SOURCE house musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 735)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
'M., Koyama, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Kouda,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,
'D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, Y., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp/
URL: http://genome-resgsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
'M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E.,
Matsumoto, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
'S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and
Hayashizaki, Y.
RIKEN Integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
'Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Aizawa
'K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome-resgsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES

Location/Qualifiers
1. 735
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A130029622"
/clone_1lb="RIKEN full-length enriched, 16 days neonate
thymus"
/tissue_type="thymus"
/dev_stage="16 days neonate"
/note="Site_1: Sali; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken

BASE COUNT 175 a 171 c 195 g 193 t 1 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 735;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 19
|||||
Db 316 AGAGCTGCCCAACTGTTT 298

RESULT 5
BH393256 796 bp DNA linear GSS 11-DEC-2001
LOCUS AG-ND-165J5.TF ND-TAM Anopheles gambiae genomic clone AG-ND-165J5.
DEFINITION DNA sequence.
ACCESSION BH393256
VERSION BH393256.1 GI:17339397
KEYWORDS GSS.
SOURCE African malaria mosquito.
ORGANISM Anopheles gambiae.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae
'1 (bases 1 to 796)
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M., and Loftus, B. J.
Direct Submission of BAC-end sequences from Anopheles gambiae
unpublished (2001)
Other GSSs: AG-ND-165J5.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@iglr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.

FEATURES
Location/Qualifiers
1. 796
/organism="Anopheles gambiae"
/db_xref="taxon:7165"
/clone="AG-ND-165J5"
/clone_1lb="ND-TAM"
/note="Vector: pCIBAC1; Site_1: HindIII"

BASE COUNT 227 a 164 c 178 g 227 t

Query Match 87.0%; Score 17.4; DB 12; Length 796;
 Best Local Similarity 94.7%; Pred. No. 2.5e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgttt 19
 |||||
 Db 762 AGAGATGCCCAACTGT 780

RESULT 6
 AL575246 627 bp mRNA linear EST 16-FEB-2001
 LOCUS AL575246 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1062YB12 5
 DEFINITION prime, mRNA sequence.

ACCESSION AL575246
 VERSION AL575246.1 GI:12936226
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 627)
 AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 Source 1..627
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1062YB12"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : filang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 146 a 175 c 130 g 158 t 18 others

Query Match 85.0%; Score 17; DB 9; Length 627;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gatgcccaactgttt 20
 |||||
 Db 59 GATGCCCAACTGT 75

RESULT 7
 AL551725 948 bp mRNA linear EST 16-FEB-2001
 LOCUS AL551725 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1062YB18 3
 DEFINITION prime, mRNA sequence.
 ACCESSION AL551725
 VERSION AL551725.1 GI:12889952
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 948)
 AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 Source 1..948
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1062YB18"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : filang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 236 a 261 c 212 g 235 t 4 others

Query Match 85.0%; Score 17; DB 9; Length 948;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gatgcccaactgttt 20
 |||||
 Db 618 GATGCCCAACTGT 634

RESULT 8
 A2766513 200 bp DNA linear GSS 16-FEB-2001
 LOCUS A2766513
 DEFINITION IM0564H07F Mouse 10kb plasmid UGCM1 library Mus musculus genomic
 clone UGCM10564H07 F, DNA sequence.
 ACCESSION A2766513
 VERSION A2766513.1 GI:12883665
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 200)
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0564 row: H column: 07
 Seq primer: CGTGTAAACGACGCCACAGT
 Class: Plasmid ends
 High quality sequence stop: 200.
 Location/Qualifiers
 1..200

FEATURES
 Source 1..200

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="MUSC1M0564H07"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PMD42nv; Purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (91473211419b|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      63 a      32 c      35 g      70 t
ORIGIN

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Query Match      84.0%; Score 16.8; DB 12; Length 200;
Best Local Similarity 90.0%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 agagatgcccaactgttt 20
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Db 137 AGAATGCCCAACTGATT 118

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RESULT 9
LOCUS AA400303 291 bp mRNA linear EST 16-MAY-1997
DEFINITION Z64803.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742732
5' mRNA sequence.
ACCESSION AA400303
VERSION AA400303.1 GI:2054192
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 291)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
T., Waterston, R., and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 205.
Location/Qualifiers
1..291
/organism="Homo sapiens"
/db_xref="GDB:5929684"
/db_xref="taxon:9606"

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FEATURES
source
1..291
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/db_xref="GDB:5929684"
/db_xref="taxon:9606"

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/clone="IMAGE:742732"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCACTGCAAGTGGAGCGCGCCCAATTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      80 a      62 c      46 g      103 t
ORIGIN

```

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Query Match      84.0%; Score 16.8; DB 9; Length 291;
Best Local Similarity 90.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 agagatgcccaactgttt 20
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Db 25 AGAGTCCCAACTGCTT 6

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RESULT 10
LOCUS BP835617 302 bp mRNA linear EST 13-JAN-2001
DEFINITION RC4-HT0890-151100-017-e11 HT0890 Homo sapiens cDNA, mRNA sequence.
ACCESSION BP835617
VERSION BP835617.1 GI:12186834
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 302)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=RC4&t=RC4-HT0890-
151100-017-e11&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 302.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0890"
/dev_stage="Adult"
/notes="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ONESTRES PCR (U.S. Letters Patent application

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TITLE
JOURNAL
MEDLINE
COMMENT

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FEATURES
source

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1..302
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0890"
/dev_stage="Adult"
/notes="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ONESTRES PCR (U.S. Letters Patent application

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ACCESSION BB508020
VERSION BB508020.1 GI:9516983
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 326)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, K., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
Y., Shigemoto, Y., Shingawa, A., Shitaki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomioka, N., Toya
T., Tsunoda, Y., Watanabe, S., Watanabe, S., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
TITLE Unpublished (2000)
JOURNAL
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagakawa, S., Sasaki
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermocyclization of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitahara, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
Y., and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome-rtc.riken.go.jp) for
further details.
FEATURES
source
Location/Qualifiers
1..326
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="D730015N05"
/clone_lib="RIKEN full-length enriched, 10 days lactation,
adult female mammary gland"
/sex="female"
/tissue_type="mammary gland"
/dev_stage="10 days lactation, adult"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGGAGAGAGCGCCGCAACTCGAGTTTCTTTTCTTTTCTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGGAGAGATCTCTGAGTATTAATTAATTAATTCCTCCCTCCCTCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FIC I."

BASE COUNT
92 a 53 c 68 g 113 t

ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 326;
Best Local Similarity 90.0%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;
Qy 1 agagatgcccaactgttt 20
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Db 72 AGAGATGCCCAACTGTTT 53

RESULT 14

D60325/c 365 bp mRNA linear EST 28-AUG-1995
LOCUS HM0099E06A Clontech human fetal brain polyA+ mRNA (#6535) Homo
DEFINITION sapiens cDNA clone GEN-099E06 3', mRNA sequence.
ACCESSION D60325.1 GI:961964
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 365)
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takachi
A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H.,
Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)
TITLE Unpublished (1995)
JOURNAL
COMMENT Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawachi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

FEATURES

source
Location/Qualifiers
1..365
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GEN-099E06"
/clone_lib="Clontech human fetal brain polyA+ mRNA (#6535
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BASE COUNT 129 a 46 c 42 g 140 t 8 others
ORIGIN

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Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 agagatgcccaactgttt 20
||||| || |||||
Db 221 AGAGATGCCCAACTGTTT 202

RESULT 15

AW879474/c 377 bp mRNA linear EST 23-MAY-2000
LOCUS PM0-OT0019-180400-003-f04 OT0019 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW879474
ACCESSION AW879474.1 GI:8041484
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 377)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

TITLE
JOURNAL
MEDLINE
COMMENT
'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=8t2=PMO-OT0019-180
400-003-f04&t3=2000-04-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence stop: 377.
Location/Qualifiers
1. 377
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="OT0019"
/dev_stage="Adult"
/note="Organ: ovary; Vector: puc18; Site: 1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

FEATURES
source

BASE COUNT 94 a 91 c 82 g 110 t
ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 377;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 agagatgcccaactgttt 20
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Db 341 AGAGACGCCCAACTGTTT 322

Search completed: September 7, 2002, 14:51:20
Job time: 16179 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2002, 01:09:16 ; Search time 1826.34 Seconds
(without alignments)
33.350 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
Sequence: 1 agagatgcccaactgtttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2036664 seqs, 1522705736 residues

Total number of hits satisfying chosen parameters: 4073328

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_MA_New:*
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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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1	20	100.0	45121	6	US-10-035-832-1262
2	17	85.0	34547	7	US-10-105-299-7482
3	16.8	84.0	251	5	US-09-975-254-17065
4	16.8	84.0	253	5	US-09-975-254-2234
5	16.8	84.0	650	7	US-10-027-632-205156
6	15.8	79.0	289	5	US-09-540-2108-20774
7	15.8	79.0	364	5	US-09-785-276A-2716
8	15.8	79.0	416	5	US-09-785-276A-11885
9	15.8	79.0	440	5	US-09-785-276A-21743
10	15.8	79.0	440	5	US-09-785-276A-22947
11	15.8	79.0	440	5	US-09-785-276A-27588
12	15.8	79.0	440	5	US-09-785-276A-28808
13	15.8	79.0	451	5	US-09-785-276A-33057
14	15.8	79.0	451	5	US-09-785-276A-41983
15	15.8	79.0	451	5	US-09-785-276A-43780
16	15.8	79.0	454	5	US-09-785-276A-13790
17	15.8	79.0	458	5	US-09-785-276A-4621
18	15.8	79.0	472	5	US-09-918-995-1867
19	15.8	79.0	482	5	US-09-918-995-1867
20	15.8	79.0	516	5	US-09-539-331D-35569
21	15.8	79.0	534	5	US-09-918-002-6997
22	15.8	79.0	864	6	US-10-098-754-20906
23	15.8	79.0	893	7	US-10-027-632-254882
24	15.8	79.0	909	5	US-09-886-492-18251
25	15.8	79.0	1157	1	PCT-US02-09188-136

C	26	15.8	79.0	1157	1	PCT-US02-09257-91	Sequence 91, App
C	27	15.8	79.0	1157	1	PCT-US02-09370-140	Sequence 140, App
C	28	15.8	79.0	1157	1	PCT-US02-09922-85	Sequence 85, App
C	29	15.8	79.0	1157	7	US-10-105-299-180	Sequence 180, App
C	30	15.8	79.0	1179	5	US-09-919-002-1295	Sequence 1295, App
C	31	15.8	79.0	1195	1	PCT-US02-23913-396	Sequence 396, App
C	32	15.8	79.0	1195	6	US-10-205-823-396	Sequence 878, App
C	33	15.8	79.0	1195	6	US-10-144-678A-878	Sequence 1, App1
C	34	15.8	79.0	1195	7	US-10-011-095-1	Sequence 1, App1
C	35	15.8	79.0	1212	7	US-10-010-667A-1	Sequence 3023, App
C	36	15.8	79.0	1294	7	US-10-179-131-3023	Sequence 112, App
C	37	15.8	79.0	1294	8	US-09-620-325-172	Sequence 45839, A
C	38	15.8	79.0	2037	8	US-60-360-039-45839	Sequence 6, App1
C	39	15.8	79.0	3627	7	US-10-011-095-6	Sequence 1214, App
C	40	15.8	79.0	3627	7	US-10-010-667A-6	Sequence 202, App
C	41	15.8	79.0	59554	6	US-10-035-832-1214	Sequence 54633, A
C	42	15.8	79.0	59554	6	US-10-052-462-202	Sequence 54634, A
C	43	15.4	77.0	25	5	US-09-396-196G-54634	Sequence 1291, App
C	44	15.4	77.0	25	5	US-09-396-196G-54634	
C	45	15.4	77.0	226	5	US-09-442-366A-1291	

ALIGNMENTS

RESULT 1
US-10-035-832-1262
; Sequence 1262, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1262
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-832-1262

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Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
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Db 8037 agagatgcccaactgtttt 8056

RESULT 2
US-10-105-299-7482/C
; Sequence 7482, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; PRIOR APPLICATION removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7482
; LENGTH: 34547
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-105-299-7482

Query Match
Best Local Similarity 85.0%; Score 17; DB 7; Length 34547;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 agatgcccacactgttt 19
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DB 30417, AGATGCCCAACTGTTT 30401

RESULT 3

US-09-975-254-17065
; Sequence 17065, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 17065
; LENGTH: 251
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700953921H1
US-09-975-254-17065

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 5; Length 251;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agaatgcccacactgttt 20
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DB 9 agaatgcccacactttt 28

RESULT 4

US-09-975-254-2234
; Sequence 2234, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 2234
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700733864H1
US-09-975-254-2234

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 5; Length 253;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agaatgcccacactgttt 20
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DB 185 agaatgcccacactttt 204

RESULT 5

US-10-027-632-205156
; Sequence 205156, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205156
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-205156

Query Match
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agaatgcccacactgttt 20
|||||
DB 70 agaatgcccacactgttt 89

RESULT 6

US-09-540-210B-20774/C
; Sequence 20774, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Sellhammer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540,210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972,899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395,244
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 08/824,029
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 60/014,010
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997

PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/903,555
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 09/862,178
PRIOR FILING DATE: May 22, 1997
PRIOR APPLICATION NUMBER: 60/018,217
PRIOR FILING DATE: May 23, 1996
PRIOR APPLICATION NUMBER: 08/881,589
PRIOR FILING DATE: June 24, 1997
PRIOR APPLICATION NUMBER: 60/021,275
PRIOR FILING DATE: June 25, 1996
PRIOR APPLICATION NUMBER: 08/903,802
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/023,308
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/905,881
PRIOR FILING DATE: August 1, 1997
PRIOR APPLICATION NUMBER: 60/025,204
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
PRIOR FILING DATE: July 30, 1997
PRIOR APPLICATION NUMBER: 60/025,478
PRIOR FILING DATE: July 31, 1996
PRIOR APPLICATION NUMBER: 08/903,556
PRIOR FILING DATE: July 31, 1997
PRIOR APPLICATION NUMBER: 60/025,217
PRIOR FILING DATE: August 22, 1996
PRIOR APPLICATION NUMBER: 08/937,142
PRIOR FILING DATE: September 23, 1997
PRIOR APPLICATION NUMBER: 60/026,598
PRIOR FILING DATE: September 24, 1996
PRIOR APPLICATION NUMBER: 08/960,746
PRIOR FILING DATE: October 29, 1997
PRIOR APPLICATION NUMBER: 60/030,144
PRIOR FILING DATE: October 30, 1996
PRIOR APPLICATION NUMBER: 08/826,847
PRIOR FILING DATE: April 10, 1997
PRIOR APPLICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR APPLICATION NUMBER: 08/755,524
PRIOR FILING DATE: November 22, 1996
PRIOR APPLICATION NUMBER: 60/007,495
PRIOR FILING DATE: November 22, 1995
PRIOR APPLICATION NUMBER: 09/021,031
PRIOR FILING DATE: February 10, 1998
PRIOR APPLICATION NUMBER: 60/039,325
PRIOR FILING DATE: February 13, 1997
PRIOR APPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: March 4, 1998
PRIOR APPLICATION NUMBER: 60/040,431
PRIOR FILING DATE: March 5, 1997
PRIOR APPLICATION NUMBER: 09/041,894
PRIOR FILING DATE: March 12, 1998
PRIOR APPLICATION NUMBER: 60/040,199
PRIOR FILING DATE: March 14, 1997
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR FILING DATE: March 30, 1998
PRIOR APPLICATION NUMBER: 60/043,792
PRIOR FILING DATE: April 11, 1997
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR APPLICATION NUMBER: 60/048,431
PRIOR FILING DATE: May 29, 1997
PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR APPLICATION NUMBER: 60/052,751
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975

PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARE: PERL Program
SEQ ID NO 20774
LENGTH: 289
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00473963
NAME/KEY: unsure
LOCATION: 31, 71, 74, 267
OTHER INFORMATION: a, t, c, g, or other
US-09-540-210B-20774

Query Match 79.0%; Score 15.8; DB 5; Length 289;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgcccaactgttt 20
|||||
DB 101 GAGATGCCCACTGTGT 83

RESULT 7
US-09-785-276A-2716
Sequence 2716, Application US/09785276A
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 2716
LENGTH: 364
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 158, 166, 285
OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-2716

Query Match 79.0%; Score 15.8; DB 5; Length 364;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgcccaactgttt 20
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DB 172 gagatgcccaactgttt 190

RESULT 8

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US-09-785-276A-11885
? Sequence 11885, Application US/09785276A
? GENERAL INFORMATION:
? APPLICANT: Schlegel, Robert
? APPLICANT: Endege, Wilson
? APPLICANT: Monahan, John
? TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
? TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
? TITLE OF INVENTION: HUMAN PROSTATE CANCER
? FILE REFERENCE: MRI-007B
? CURRENT APPLICATION NUMBER: US/09/785,276A
? CURRENT FILING DATE: 2001-02-16
? PRIOR APPLICATION NUMBER: 60/183,319
? PRIOR FILING DATE: 2000-02-17
? PRIOR APPLICATION NUMBER: 60/189,862
? PRIOR FILING DATE: 2000-03-16
? PRIOR APPLICATION NUMBER: 60/207,454
? PRIOR FILING DATE: 2000-05-25
? PRIOR APPLICATION NUMBER: 60/211,314
? PRIOR FILING DATE: 2000-06-09
? PRIOR APPLICATION NUMBER: 60/219,007
? PRIOR FILING DATE: 2000-07-18
? PRIOR APPLICATION NUMBER: 60/255,281
? PRIOR FILING DATE: 2000-12-13
? NUMBER OF SEQ ID NOS: 62232
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 11885
? LENGTH: 416
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-785-276A-11885

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	Query Match	79.0%	Score 15.8;	DB 5;	Length 416;
	Best Local Similarity	89.5%;	Pred. No. 1.6e+02;		
	Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
Oy	2 gagatgcccaactgcgttctt	20			
Db	137 gagaagcccaactgcgttctt	155			

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RESULT 9
US-09-785-2176A-21743/c
; Sequence 21743; Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21743
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens

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Best Local Similarity	89.5%;	Pred. No. 1.6e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
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Db	308	GAGAA GCCCAACTGCTTT	290	

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RESULT 10
US-09-785-276A-22947/C
; Sequence 22947, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007H
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/785, 276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183, 319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189, 862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207, 454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211, 314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219, 007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255, 281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 22947
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-22947

```

```

Query Match      79.0%; Score 15.8; DB 5; Length 440;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0
OY      2 gagatgcccaactgttt 20
      ||||| ||||| ||||| |||
Db      308 GAGAGGCCCAACTGCTTT 290

RESULT 11
US-09-785-276A-27588/c
; Sequence 27588, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454

```

```

; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27588
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-27588

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```

Query Match          79.0%; Score 15.8; DB 5; Length 440;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 2 gagatgcccaactgtttt 20
    ||| ||||| ||||| |||
Db 308 GAGAAGCCCAACTGCTTT 290

```

```

RESULT 12
; Sequence 28808, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28808
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-28808

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```

Query Match          79.0%; Score 15.8; DB 5; Length 440;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 2 gagatgcccaactgtttt 20
    ||| ||||| ||||| |||
Db 308 GAGAAGCCCAACTGCTTT 290

```

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RESULT 13
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; Sequence 33057, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert

```

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; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33057
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-33057

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Query Match          79.0%; Score 15.8; DB 5; Length 451;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 2 gagatgcccaactgtttt 20
    ||| ||||| ||||| |||
Db 174 gagatgcccaactgttt 192

```

```

RESULT 14
; Sequence 41983, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41983
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-41983

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Query Match          79.0%; Score 15.8; DB 5; Length 451;

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Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgccaactgtttt 20
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Db 174 gagaagccaactgtttt 192

RESULT 15
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; Sequence 43780, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785, 276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43780
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-43780

Query Match 79.0%; Score 15.8; DB 5; Length 451;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgccaactgtttt 20
||| ||||| |||
Db 174 gagaagccaactgtttt 192

Search completed: September 8, 2002, 01:09:18
Job time: 37036 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:30:49 ; Search time 13836.9 Seconds
(without alignments)
31.271 Million cell updates/sec

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Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	40	32	US-09-834-291-26
4	20	100.0	2827	32	US-09-834-291-4
5	20	100.0	3212	32	US-09-834-291-1
6	20	100.0	732	34	US-09-897-722-10
7	17.4	87.0	26460	19	US-09-910-943-719
8	17.4	87.0	1230230	18	US-09-528-2378-596
9	17.4	87.0	1230230	18	US-09-438-185-1
10	17.4	85.0	1501	31	US-09-438-185A-1
11	17	85.0	7865	21	US-09-815-264-56014
12	17	85.0	7865	28	US-09-620-392-50130
13	17	85.0	7865	24	US-09-702-134-2703
14	17	85.0	7865	31	US-09-815-264-82703
15	17	85.0	34547	35	US-09-950-083-5371
16	17	85.0	176251	63	US-60-248-505-361
17	17	85.0	236630	63	US-60-248-505-158
18	16.8	84.0	20	32	US-09-834-291-13
19	16.8	84.0	201	36	US-09-244-000A-53774
20	16.8	84.0	201	36	US-09-978-703-53774
21	16.8	84.0	234	1	PCT-US02-03987-3905
22	16.8	84.0	234	31	US-09-815-242-3905
23	16.8	84.0	234	37	US-10-072-851-3905
24	16.8	84.0	250	16	US-09-283-466-6288
25	16.8	84.0	251	16	US-09-263-191-17065
26	16.8	84.0	251	27	US-09-654-617-108604
27	16.8	84.0	251	27	US-09-684-016-108604
28	16.8	84.0	253	16	US-09-263-191-2234
29	16.8	84.0	255	16	US-09-283-466-6446
30	16.8	84.0	267	11	US-08-766-606-458
31	16.8	84.0	267	13	US-08-979-854A-458

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32 16.8 84.0 267 21 US-09-540-229-21936 Sequence 21936, A
33 16.8 84.0 269 16 US-09-283-466-6496 Sequence 6496, A
34 16.8 84.0 293 51 US-60-125-818-6768 Sequence 6768, Ap
35 16.8 84.0 306 1 PCT-US02-03987-6707 Sequence 6707, Ap
36 16.8 84.0 306 31 US-09-815-242-6707 Sequence 6707, Ap
37 16.8 84.0 306 37 US-10-072-851-6707 Sequence 6707, Ap
38 16.8 84.0 312 8 US-08-438-571A-341 Sequence 341, Appl
39 16.8 84.0 320 17 US-09-342-216-31 Sequence 31, Appl
40 16.8 84.0 320 17 US-09-342-216A-31 Sequence 31, Appl
41 16.8 84.0 320 34 US-09-908-601-31 Sequence 31, Appl
42 16.8 84.0 320 34 US-09-912-292-1183 Sequence 1183, Ap
43 16.8 84.0 321 15 US-09-134-000-2304 Sequence 2304, Ap
44 16.8 84.0 366 36 US-09-974-300-1452 Sequence 1452, Ap
45 16.8 84.0 386 17 US-09-304-517A-249988 Sequence 249988,

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ALIGNMENTS

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RESULT 1
US-09-834-291-12
; Sequence 12, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-12

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Query Match 100.0%; Score 20; DB 32; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 agagatgcccaactgtttt 20
Db 1 agagatgcccaactgtttt 20

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RESULT 2
US-09-834-291-18
; Sequence 18, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo Sapiens

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US-09-834-291-18

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Query Match 100.0%; Score 20; DB 32; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 agagatgcccaactgtttt 20
Db 11 agagatgcccaactgtttt 30

```

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RESULT 3
US-09-834-291-26
; Sequence 26, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-26

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Query Match 100.0%; Score 20; DB 32; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 agagatgcccaactgtttt 20
Db 11 agagatgcccaactgtttt 30

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RESULT 4
US-09-834-291-4
; Sequence 4, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4

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Query Match 100.0%; Score 20; DB 32; Length 2827;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 44 agagatgcccaactgttt 63

RESULT 5
US-09-834-291-1
; Sequence 1, Application US/09834291
; GENERAL INFORMATION:

APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIORITY APPLICATION NUMBER: PCT/DE99/03343
PRIORITY FILING DATE: 1999-10-18
PRIORITY APPLICATION NUMBER: DE 198 47 779.1
PRIORITY FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1
LENGTH: 3212
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match 100.0%; Score 20; DB 32; Length 3212;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agagatgcccaactgttt 20
|||||
Db 44 agagatgcccaactgttt 63

RESULT 6
US-09-997-722-10
; Sequence 10, Application US/09997722
; GENERAL INFORMATION:

APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIORITY APPLICATION NUMBER: US 09/747,377
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US 09/798,586
PRIORITY FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1

SEQ ID NO 10
LENGTH: 45121
TYPE: DNA
ORGANISM: Homo sapiens
US-09-997-722-10

Query Match 100.0%; Score 20; DB 36; Length 45121;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agagatgcccaactgttt 20
|||||
Db 8037 agagatgcccaactgttt 8056

RESULT 7
US-09-910-943-719/C
; Sequence 719, Application US/09910943

GENERAL INFORMATION:
APPLICANT: Hemmati-Brivanlou, Ali

APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/1G1480S1
CURRENT APPLICATION NUMBER: US/09/910,943
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 742
SOFTWARE: PatentIn version 3.1
SEQ ID NO 719
LENGTH: 732
TYPE: DNA
ORGANISM: Xenopus laevis
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(732)
OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-719

Query Match 87.0%; Score 17.4; DB 34; Length 732;
Best Local Similarity 94.7%; Pred. No. 3,1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 gagatgcccaactgttt 20
|||||
Db 101 gagatgcccaactgttt 83

RESULT 8
US-09-528-237A-596/C
; Sequence 596, Application US/09528237A
; GENERAL INFORMATION:

APPLICANT: Venter, J. Craig
TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
TITLE OF INVENTION: Sequences and Uses Thereof
FILE REFERENCE: CL000284
CURRENT APPLICATION NUMBER: US/09/528,237A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 2926
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 596
LENGTH: 26460
TYPE: DNA
ORGANISM: Drosophila
US-09-528-237A-596

Query Match 87.0%; Score 17.4; DB 19; Length 26460;
Best Local Similarity 94.7%; Pred. No. 6,4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 agagatgcccaactgttt 19
|||||
Db 23498 agagatgcccaactgttt 23480

RESULT 9
US-09-438-185-1/C
; Sequence 1, Application US/09438185
; GENERAL INFORMATION:

APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kaiman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185
CURRENT FILING DATE: 1999-11-11
PRIORITY APPLICATION NUMBER: US 60/108,279
PRIORITY FILING DATE: 1998-11-12

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;; PRIOR APPLICATION NUMBER: US 60/128,606
;; PRIOR FILING DATE: 1999-04-08
;; NUMBER OF SEQ ID NOS: 1074
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1
;; LENGTH: 1230230
;; TYPE: DNA
;; ORGANISM: Chlamydia pneumoniae
US-09-438-185-1
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Query Match
Best Local Similarity 87.0%; Score 17.4; DB 18; Length 1230230;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1024745 GAGATGCCCAAACTGTTT 1024727
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RESULT 10
US-09-438-185A-1/c
; Sequence 1. Application US/09438185A
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1230230
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1
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Query Match
Best Local Similarity 87.0%; Score 17.4; DB 18; Length 1230230;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1024745 GAGATGCCCAAACTGTTT 1024727
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RESULT 11
US-09-815-264-56014/c
; Sequence 56014, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dolson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
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;; PRIOR APPLICATION NUMBER: US 09/702,134
;; PRIOR FILING DATE: 2000-10-31
;; NUMBER OF SEQ ID NOS: 109669
;; SEQ ID NO 56014
;; LENGTH: 1501
;; TYPE: DNA
;; ORGANISM: Oryza sativa
US-09-815-264-56014
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Query Match
Best Local Similarity 85.0%; Score 17; DB 31; Length 1501;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 926 AGATGCCCAAACTGTTT 910
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RESULT 12
US-09-620-392-50130/c
; Sequence 50130, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 50130
; LENGTH: 7865
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-50130
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Query Match
Best Local Similarity 85.0%; Score 17; DB 24; Length 7865;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1445 AGATGCCCAAACTGTTT 1429
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RESULT 13
US-09-702-134-2703/c
; Sequence 2703, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 2703
; LENGTH: 7865
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-2703
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Query Match
Best Local Similarity 85.0%; Score 17; DB 28; Length 7865;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 PRIOR FILING DATE: 1999-03-12
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 PRIOR APPLICATION NUMBER: US 60/124,145
 PRIOR FILING DATE: 1999-03-12
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 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/168,661
 PRIOR FILING DATE: 1999-12-03
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 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/168,622
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,143
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/168,663
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,095
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/138,598
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: US 60/168,665

PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/125,360
 PRIOR FILING DATE: 1999-03-19
 PRIOR APPLICATION NUMBER: US 60/138,626
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: US 60/168,662
 PRIOR FILING DATE: 1999-12-03
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 PRIOR APPLICATION NUMBER: US 60/168,667
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/124,142
 PRIOR FILING DATE: 1999-03-12
 PRIOR APPLICATION NUMBER: US 60/138,597
 PRIOR FILING DATE: 1999-06-11
 PRIOR APPLICATION NUMBER: US 60/168,666
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/125,359
 PRIOR FILING DATE: 1999-03-19
 PRIOR APPLICATION NUMBER: US 60/168,664
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: US 60/126,051
 PRIOR FILING DATE: 1999-03-23
 PRIOR APPLICATION NUMBER: US 60/169,906

Query Match 85.0%; Score 17; DB 35; Length 34547;
 Best Local Similarity 100.0%; Pred. No. 11e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 agatgcccaactgtt 19
 Db 30417 AGATGCCCAACTGTT 30401

Search completed: September 7, 2002, 22:31:31
 Job time: 43785 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:05 ; Search time 212.3 Seconds
(without alignments)
23.140 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
Sequence: 1 agagatgcccaactgtttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	16.8	84.0	43795 3	US-08-742-185-101
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4	15.8	79.0	3627 4	US-09-323-873A-6
5	15.4	77.0	1644 3	US-07-903-047-7
6	15.4	77.0	1644 3	US-09-111-752-13
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16	14.8	74.0	26664 4	US-09-564-805-28
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29	14.4	72.0	9103 2	US-08-464-134-182	Sequence 182, App
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35	14.2	71.0	660 3	US-09-284-782-15	Sequence 104, App
36	14.2	71.0	756 5	PCT-US96-03940-2	Sequence 52, App
37	14.2	71.0	957 4	US-08-858-207A-104	Sequence 28, App
38	14.2	71.0	1067 4	US-09-058-368-6	Sequence 3, App
39	14.2	71.0	1255 4	US-09-227-357-52	Sequence 27, App
40	14.2	71.0	1284 5	PCT-US96-03940-28	Sequence 10, App
41	14.2	71.0	1407 5	PCT-US96-03940-27	Sequence 3, App
42	14.2	71.0	1461 5	US-09-657-042A-10	Sequence 14, App
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ALIGNMENTS

RESULT 1
US-08-578-634C-3/C
Sequence 3, Application US/08578634C
Patent No. 6025163
GENERAL INFORMATION:
APPLICANT: Vladimir Shamanin
APPLICANT: Ethel Michele De Villiers
APPLICANT: Zuer Hausen
APPLICANT: Irene Leigh
APPLICANT: Harald Zur Hausen
TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA
NUMBER OF SEQUENCES: 9
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578, 634C
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8484-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-4935
TELEFAX: (650) 493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1.. 660

US-08-578-634C-3

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 3; Length 661;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 20
Db 567 AGAGTGTGCCCAAGTCTTT 548

RESULT 2

US-08-742-185-101
Sequence 101, Application US/08742185
Patent No. 6020476
GENERAL INFORMATION:
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 43795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match

Best Local Similarity 90.0%; Score 16.8; DB 3; Length 43795;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 agagatgcccaactgtttt 20
Db 22516 AGAGTGTGCCCAAGTCTTT 22535

RESULT 3

US-09-323-873A-1/c
Sequence 1, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE REFERENCE: 129,16US02
CURRENT APPLICATION NUMBER: US/09/323,873A
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-323-873A-1

Query Match

Best Local Similarity 79.0%; Score 15.8; DB 4; Length 1195;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgcccaactgtttt 20
Db 566 GAGAAGCCCAACTGCTTT 548

RESULT 4

US-09-323-873A-6/c
Sequence 6, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE REFERENCE: 129,16US02
CURRENT APPLICATION NUMBER: US/09/323,873A
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-323-873A-6

Query Match

Best Local Similarity 79.0%; Score 15.8; DB 4; Length 3627;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagatgcccaactgtttt 20
Db 596 GAGAAGCCCAACTGCTTT 578

RESULT 5
US-07-903-047-7/c
Sequence 7, Application US/07903047
Patent No. 5229285
GENERAL INFORMATION:
APPLICANT: Kajiya, Naoki
TITLE OF INVENTION: Thermostable Luciferase Gene Of Firefly, No. 5229285el Recombi
TITLE OF INVENTION: DNA, And Process For The Preparation Of Thermostable
TITLE OF INVENTION: Luciferase Of Firefly
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue Of The Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903.047
FILING DATE: 19920623
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
US-07-903-047-7

Query Match 77.0%; Score 15.4; DB 1; Length 1644;
Best local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 agagatgcccaactgt 17
|||||
Db 369 AGAGATGCCCTAACTGT 353

RESULT 6
US-09-111-752-13/c
Sequence 13, Application US/09111752
Patent No. 6074859
GENERAL INFORMATION:
APPLICANT: HIROKAWA, KOZO
APPLICANT: KAJIYAMA, NAOKI
APPLICANT: MURAKAMI, SEIJI
TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND
TITLE OF INVENTION: PROCESS FOR PRODUCING MUTANT-TYPE LUMINESCENT PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON

STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111.752
FILING DATE: 08-JUL-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-0009-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Luciola lateralis
US-09-111-752-13

Query Match 77.0%; Score 15.4; DB 3; Length 1644;
Best local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 agagatgcccaactgt 17
|||||
Db 369 AGAGATGCCCTAACTGT 353

RESULT 7
US-09-380-061B-15/c
Sequence 15, Application US/09380061B
Patent No. 6265177
GENERAL INFORMATION:
APPLICANT: SQUIRELL, DAVID JAMES
WHITE, PETER JOHN
LOWE, CHRISTOPHER ROBIN
MURRAY, JAMES AUGUSTUS HENRY
TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380.061B
FILING DATE: 25-AUG-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01026
FILING DATE: 7-APR-1998
APPLICATION NUMBER: GB 9707468.8
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 124-725
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1644
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-380-061B-15

Query Match 77.0%; Score 15.4; DB 4; Length 1644;
Best Local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccactgt 17
|||||||
Db 369 AGAGATGCGCTAACTGT 353

RESULT 8
US-08-460-934-5/c
Sequence 5, Application US/08460934
Patent No. 5814465
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,934
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
NAME/KEY: misc feature
LOCATION: 1..1704
OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombinant plasmid pHLf203 DNA
OTHER INFORMATION: plasmid pHLf203 DNA
US-08-460-934-5

Query Match 77.0%; Score 15.4; DB 1; Length 1704;
Best Local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccactgt 17
|||||||
Db 429 AGAGATGCGCTAACTGT 413

RESULT 9
US-08-782-118-5/c
Sequence 5, Application US/08782118
Patent No. 5843746
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,118
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/460,934
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995

GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOTAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,118
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/460,934
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..1908
OTHER INFORMATION: /note="The nucleotide sequence of
OTHER INFORMATION: the biotinylated firefly luciferase gene contained in
FEATURE: recombinant plasmid pHLf248 DNA"
NAME/KEY: CDS
LOCATION: 1..1908
US-08-782-118-8

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 2; Length 1908;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtt 17
|||||
Db 369 AGAGATGCCCTAACTGT 353

RESULT 12
US-08-578-634C-2/c
Sequence 2, Application US/08578634C
Patent No. 6025163
GENERAL INFORMATION:
APPLICANT: Vladimir Shamanin
APPLICANT: Ethel Michele De Villiers
APPLICANT: Irene Leigh
APPLICANT: Harald Zur Hausen
TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA
TITLE OF INVENTION: VIRUS MAIN CAPSIDE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penite & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,634C
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8484-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-4935
TELEFAX: (650) 493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..666
US-08-578-634C-2

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 668;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtt 20
|||||
Db 567 AGAGTACCCCAAGTGT 548

RESULT 13
US-09-109-204-20/c
Sequence 20, Application US/09109204
Patent No. 6060250
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocycle Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:

LENGTH: 495 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TESTNOT04
CLONE: 301251r6
US-09-109-204-20

Query Match 74.0%; Score 14.8; DB 3; Length 495;
Best Local Similarity 88.9%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 agatgcccaactgttt 20
||||| ||||| ||||| ||
Db 345 AGATGCCCAACTGTATT 328

RESULT 14

US-09-109-204-19
Sequence 19, Application US/09109204
Patent No. 6060250

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: N/A
CLONE: SAGA01614F1
US-09-109-204-19

Query Match 74.0%; Score 14.8; DB 3; Length 605;

Best Local Similarity 88.9%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 agatgcccaactgttt 20
||||| ||||| ||||| ||
Db 537 AGATGCCCAACTGTATT 554

RESULT 15

US-09-109-204-5
Sequence 5, Application US/09109204
Patent No. 6060250

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOT09
CLONE: 2150892
US-09-109-204-5

Query Match 74.0%; Score 14.8; DB 3; Length 2125;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 agatgcccaactgttt 20
||||| ||||| ||||| ||
Db 1780 AGATGCCCAACTGTATT 1797

Search completed: September 7, 2002, 18:21:07
Job time: 28761 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:39:36 : Search time 1139.19 Seconds
(without alignments)
30.143 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
Perfect score: 20
Sequence: 1 agagatgcccaacacgtttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N-Geneseq_032802:*

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- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.*
- 7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.*
- 16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.*
- 17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1996.DAT.*
- 18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	AAZ88701	Human CD95 recepto
2	16.8	84.0	234	AAS51323	Enterococcus faeca
3	16.8	84.0	306	AAS53070	Enterococcus faeca
4	16.8	84.0	338	AAC18125	Human secreted pro
5	16.8	84.0	661	AAV39501	Papilloma virus ma
6	16.8	84.0	2008	AAV39297	Human RAD54 nuclei
7	16.8	84.0	3001	AAH51750	Chromosome 13q31-q
8	16.8	84.0	9821	AAI03245	Human reproductive
9	16.8	84.0	9824	AAI03246	Human reproductive

10	16.8	84.0	20072	20	AAI13026	Enterococcus faeca
11	16.8	84.0	43795	21	AAZ292583	Human DAZ genomic
12	16.8	84.0	349980	22	AAH41226	Pyrococcus abyssi
13	16.4	82.0	396	22	AAH99123	Human EST-derived
14	15.8	79.0	1157	22	AAH63808	Human secreted pro
15	15.8	79.0	1193	21	AAZ49395	Human STRAP-1 CDNA
16	15.8	79.0	1193	22	AAZ49395	Human six transmem
17	15.8	79.0	1195	22	AAH39924	Human prostate CDN
18	15.8	79.0	1195	22	AAH39924	Human prostate CDN
19	15.8	79.0	1227	23	AAH39924	Human prostate CDN
20	15.8	79.0	1229	22	AAH39924	Human prostate CDN
21	15.8	79.0	1294	22	AAH39924	Human prostate CDN
22	15.8	79.0	2005	23	AAH39924	Human prostate CDN
23	15.8	79.0	2108	24	AAH39924	Human prostate CDN
24	15.8	79.0	2516	23	AAH39924	Human prostate CDN
25	15.8	79.0	2757	24	AAH39924	Human prostate CDN
26	15.8	79.0	3123	23	AAH39924	Human prostate CDN
27	15.8	79.0	3627	21	AAZ49395	Human six transmem
28	15.8	79.0	4005	23	AAH39924	Human prostate CDN
29	15.8	79.0	4005	23	AAH39924	Human prostate CDN
30	15.8	79.0	16989	23	AAH39924	Human prostate CDN
31	15.8	79.0	16989	23	AAH39924	Human prostate CDN
32	15.8	79.0	32172	22	AAH39924	Human prostate CDN
33	15.4	77.0	150	21	AAH39924	Human six transmem
34	15.4	77.0	496	22	AAH39924	Human prostate CDN
35	15.4	77.0	1644	11	AAH39924	Human prostate CDN
36	15.4	77.0	1644	14	AAH39924	Human prostate CDN
37	15.4	77.0	1644	20	AAH39924	Human prostate CDN
38	15.4	77.0	1644	20	AAH39924	Human prostate CDN
39	15.4	77.0	1644	20	AAH39924	Human prostate CDN
40	15.4	77.0	1656	20	AAH39924	Human prostate CDN
41	15.4	77.0	1704	18	AAH39924	Human prostate CDN
42	15.4	77.0	1704	19	AAH39924	Human prostate CDN
43	15.4	77.0	1908	18	AAH39924	Human prostate CDN
44	15.4	77.0	1920	19	AAH39924	Human prostate CDN
45	15.4	77.0	2019	17	AAH39924	Human prostate CDN

ALIGNMENTS

RESULT 1
ID AAZ88701 standard; DNA; 20 BP.
AC AAZ88701;
DT 11-MAY-2000 (first entry)
DE Human CD95 receptor promoter DNA p53 binding fragment #1.
XX
DE
XX
KW p53; CD95 receptor; human; screening; apoptosis-modulation;
KW cancer chemotherapy; ss.
XX
OS Homo sapiens.
XX
PM DE19847779-C1.
XX
PD 03-FEB-2000.
XX
PF 16-OCT-1998; 98DE-1047779.
XX
PR 16-OCT-1998; 98DE-1047779.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Krammer P, Mueller-Schilling M, Oren M;
XX WPI: 2000-162245/15.
XX
XX Novel receptor DNA useful for identifying apoptosis-modulating
XX substances potentially useful for cancer chemotherapy

PS Claim 2; Fig 5; 12pp; German.

CC This invention describes a novel p53-binding region of a human CD95
CC receptor DNA molecule. The p53-binding region, or a vector containing
CC it, can be used to screen for apoptosis-modulating substances
CC potentially useful for cancer chemotherapy. This sequence represents a
CC fragment of the human CD95 receptor promoter which is capable of
CC binding p53.

XX Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 20; DB 21; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 1 agagatgcccaactgtttt 20

RESULT 2

AA551323/c
ID AA551323 standard; DNA: 234 BP.

AC AA551323;

DT 13-FEB-2002 (first entry)

DE Enterococcus faecalis DNA for cellular proliferation protein #100.

KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.

OS Enterococcus faecalis.

PN WO200170955-A2.

XX 27-SEP-2001.

PD 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2001; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR P-PSDB; AAU33464.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

PS Claim 27; Seq ID No 3905; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC and to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 234 BP; 84 A; 33 C; 46 G; 71 T; 0 other;

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 23; Length 234;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 87 AGAATGCACCAACTGTTT 68

RESULT 3

AA553070/c
ID AA553070 standard; DNA: 306 BP.

AC AA553070;

DT 13-FEB-2002 (first entry)

DE Enterococcus faecalis DNA for cellular proliferation protein #498.

KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.

OS Enterococcus faecalis.

PN WO200170955-A2.

XX 27-SEP-2001.

PD 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2001; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR P-PSDB; AAU35211.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

PS Claim 27; Seq ID No 6707; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC and to identify proteins used in proliferation, to express these proteins,

ID AAV39297 standard; CDNA; 2008 BP.
XX AAV39297;
AC
XX 16-SEP-1998 (first entry)
DT
XX
DE Human RAD54 nucleic acid sequence comprising exons 5-8.
XX
XX Human; RAD54; hrRAD54; cancer; xeroderma pigmentosum; Bloom syndrome;
KW Werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily;
KM X-linked mental retardation with alpha-thalassemia syndrome; tumour;
XX gene therapy; ss.
XX
OS Homo sapiens.
XX
XX EP844305-A2.
PN
XX 27-MAY-1998.
PD
XX
PF 10-NOV-1997; 97EP-0308998.
PR
XX 13-NOV-1996; 96US-0030676.
XX
PA (SMR) SMITHKLINE BEECHAM CORP.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Croce CM, Fishel RA, Rasio D, Robbins DJ;
PI WPI; 1998-274189/25.
DR
XX
XX Human hrRAD54 DNA and polypeptide - and agonists, antibodies,
PT antagonists, etc.
XX
XX
PS Claim 1; Page 27-28; 64pp; English.
XX
XX
CC The present sequence represents a specifically claimed partial nucleic
CC acid sequence encoding human RAD54 (hrRAD54). A method for analysing a
CC sample for mutation of DNA encoding hrRAD54 has been developed using a
CC DNA sequence of at least 15 and no more than 30 consecutive bases of
CC the DNA sequence encoding hrRAD54. hrRAD54 is a gene thought to be present
CC in tumours that display allelic imbalance at 1p32, the chromosomal band
CC identified as one of four minimal regions of chromosome 1 deletion in
CC breast carcinomas. hrRAD54 is useful for production of proteins, inter
CC alia, that have been identified as novel hrRAD54 by homology between the
CC amino acid sequence given in AAM62186 and known amino acid sequences
CC such as yeast RAD54. hrRAD54 is used in the treatment of
CC cancer, including Xeroderma pigmentosum and Bloom syndrome, Werner's
CC syndrome and X-linked mental retardation with alpha-thalassemia
CC detecting complementary nucleotides for use as a diagnostic agent, for
CC especially useful for diagnosis of disease or susceptibility to diseases.
CC hrRAD54 polynucleotide, proteins, agonists and antagonists which are
CC proteins are useful in gene therapy.
XX
XX Sequence 2008 BP; 489 A; 419 C; 570 G; 526 T; 4 other;
SQ

Query Match 84.0%; Score 16.8; DB 19; Length 2008;
Best Local Similarity 90.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 agagatgcccaactgtttt 20
DB 139 agagatgcccaactgtt 158

RESULT 7
AAH51750/c
ID AAH51750 standard; DNA; 3001 BP.
XX
XX AAH51750;
AC
XX
DT 29-AUG-2001 (first entry)

XX
XX Chromosome 13q31-q33 biallelic marker containing amplicon SEQ ID 162.
XX
XX sbg1; g34665; sbg2; g35017; g35018; chromosome 13q31-q33; haplotype;
KW biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200058510-A2.
PN
XX
XX 05-OCT-2000.
PD
XX
XX 30-MAR-2000; 2000WO-IB00435.
PF
XX
XX 30-MAR-1999; 99US-0126903.
PR 30-APR-1999; 99US-0131971.
PR 30-APR-1999; 99US-0132065.
PR 14-JUL-1999; 99US-0143928.
PR 27-JUL-1999; 99US-0145915.
PR 29-JUL-1999; 99US-0146452.
PR 29-JUL-1999; 99US-0146453.
PR 28-OCT-1999; 99US-0162288.
XX
XX (GENSET) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I, Bougueleret L, Bihain B;
PI Essioux L;
XX
XX WPI; 2000-619082/59.
DR
XX
XX
XX Polynucleotides comprising sequences from sbg1 and g35018 biallelic
PT markers are used for genotyping and detecting schizophrenia or bipolar
PT disorder and predisposition to these disorders -
XX
XX
XX Claim 2; Page 643-644; 737pp; English.
XX
XX
XX AAH51601 represents a human genomic nucleotide sequence comprising sbg1,
XX g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the
XX human chromosome 13q31-q33 locus. The nucleotide sequences contain
XX biallelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and
XX AAB62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and protein
XX products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018
XX cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used
XX to isolate sbg1 cDNAs, while sbg1 exons from different primates are
XX represented by sequences AAH51642 - AAH51699. Nucleotide sequences of
XX amplicons which comprise biallelic markers located on the chromosome
XX 13q31-q33 locus are represented in AAH51700 - AAH51817. Biallelic markers
XX are represented in the sequences by degenerate/undefined base codes. PCR
XX primers AAH51818 and AAH51819 are used in the isolation of sequences of
XX the invention. The biallelic marker containing nucleotide sequences are
XX used to determine the identity of the nucleotide at a biallelic marker in
XX a sample DNA sequence. The nucleotide sequences may be labelled and used
XX for genotyping by determining the identity of a nucleotide at a Region
XX D-related biallelic marker in a biological sample from single or multiple
XX subjects. By determining the frequency of a biallelic marker in a
XX population an association between a genotype and a trait, a haplotype and
XX a trait and a phenotype and a trait can be detected. The sequences can be
XX used to determine a predisposition to or early onset of schizophrenia or
XX bipolar disorder or a beneficial response to or side effects related to
XX treatment against schizophrenia or bipolar disorder.
SQ
XX
XX Sequence 3001 BP; 842 A; 608 C; 584 G; 966 T; 1 other;
SQ

Query Match 84.0%; Score 16.8; DB 21; Length 3001;
Best Local Similarity 90.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 agagatgcccaactgtttt 20
DB 427 agagatgcccaactgtt 408

RESULT 8
AAL03245/C
ID AAL03245 standard; DNA: 9821 BP.
XX
AC AAL03245;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5933.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
XX
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN W0200155320-A2.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01339.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226888.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227189.
PR 30-AUG-2000; 2000US-0228284.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231248.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231966.

PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 29-SEP-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239937.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0244617.
PR 01-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.

PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMAN-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX
PS Disclosure; SEQ ID NO 5933; 1297bp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
XX
SQ Sequence 9821 BP; 3056 A; 1735 C; 1689 G; 3341 T; 0 other;

Query Match 84.0%; Score 16.8; DB 22; Length 9821;
Best Local Similarity 90.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 agagatgcccaactgtttt 20
||| ||||| ||||| |||
Db 2800 AGAGCTGCCCAACTGCTT 2781

RESULT 9
AAL03246/C
ID AAL03246 standard; DNA; 9824 BP.
XX
AC AAL03246;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5934.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX MO200155320-A2.
XX
XX PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001MO-US01339.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 02-MAR-2000; 2000US-0184664.
XX 16-MAR-2000; 2000US-0186350.
XX 17-MAR-2000; 2000US-0189874.
XX 18-APR-2000; 2000US-0190076.
XX 19-MAY-2000; 2000US-0198123.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.
PR 22-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227009.
PR 01-SEP-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 25-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 26-SEP-2000; 2000US-0234998.
PR 27-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 20-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.

PR	20-OCT-2000	2000US-0241808	
PR	20-OCT-2000	2000US-0241809	
PR	20-OCT-2000	2000US-0241826	
PR	01-NOV-2000	2000US-0241617	
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PR	01-DEC-2000	2000US-0250160	
PR	01-DEC-2000	2000US-0250391	
PR	05-DEC-2000	2000US-0251030	
PR	05-DEC-2000	2000US-0251033	
PR	05-DEC-2000	2000US-0256719	
PR	05-DEC-2000	2000US-0256720	
PR	06-DEC-2000	2000US-0251479	
PR	06-DEC-2000	2000US-0251856	
PR	08-DEC-2000	2000US-0251868	
PR	08-DEC-2000	2000US-0251869	
PR	08-DEC-2000	2000US-0251989	
PR	08-DEC-2000	2000US-0251990	
PR	11-DEC-2000	2000US-0254097	
PR	05-JAN-2001	2001US-0259678	
XX			
XX			
PA	(HUMA-)	HUMAN GENOME SCI INC.	
XX			
PI	Rosen CA, Barash SC, Ruben SM.		
XX			
DR	WPI: 2001-46570/50.		
XX			
XX			
PT	Isolated nucleic acid molecule encoding a reproductive system antigen		
PT	is used in preventing, treating or ameliorating a medical condition		
XX			
XX			
PS	Disclosure: SEQ ID NO 5934; 1297bp + Sequence Listing; English.		
XX			
CC	The present invention provides the protein and coding sequences of a		
CC	number of human reproductive system related antigens. These can be used		
CC	in the prevention and treatment of reproductive system disorders,		
CC	including cancer. The present sequence is a genomic sequence encoding a		
CC	protein of the invention.		

	Query Match	84.0%;	Score 16.8;	DB 22;	Length 9824;	
	Best Local Similarity	90.0%;	Pred. No. 74;			
	Matches 18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
OY	1 agagatgcccaactgtttt 20 					
Dn	2800 AGAGCTGCCCAAACTGCTT 2781					
	RESULT 10					
ID	AAI3026					
XX	AAAI3026 standard; DNA; 20072 BP.					
AC	AAI3026;					
XX						
DT	19-MAR-1999 (first entry)					
XX						
DE	Enterococcus faecalis genome contig SEQ ID NO:89.					
XX						
KW	Enterococcus faecalis; contig; detection; Enterococcal infection;					
XX	vaccine; attenuation; computer readable medium; ds.					
OS	Enterococcus faecalis.					
PN	WO9850555-A2.					
XX						
PD	12-NOV-1998.					
PF	04-MAY-1998; 98WO-US08985.					
PR	14-NOV-1997; 97US-0066009.					
PR	06-MAY-1997; 97US-0044031.					
PR	16-MAY-1997; 97US-0046655.					
XX						
PA	(HUMA-) HUMAN GENOME SCI INC.					
XX						
PI	Barash SC, Dillon PJ, Kunsch CA;					
DR	WPI: 1999-045171/04.					
XX						
PT	New isolated Enterococcus faecalis polynucleotides and polypeptides					
PT	- used to develop products for the detection of Enterococcus and for					
PT	use in vaccines for prevention or attenuation of Enterococcus					
PT	infection.					
XX						
PS	Claim 1; Page 596-606; 2084pp; English.					
XX						
CC	A computer readable medium has been developed which has recorded on it					
CC	992 nucleotide sequences isolated from the Enterococcus faecalis genome.					
CC	AXAI2938 to AXAI3319 represent these nucleotide sequences which are					
CC	primary nucleotide sequences, also known as contigs. The computer-based					
CC	system can identify fragments of the Enterococcus faecalis genome with					
CC	commercial importance. The products can be used to detect the presence					
CC	of Enterococcus faecalis in samples. They can also be used for					
CC	diagnosing Enterococcal infection in an animal and monitoring					
CC	progression of disease, and for identifying agents which can be used to					
CC	modulate the growth or pathogenicity of Enterococcus faecalis, or					
CC	another related organism, in vivo or in vitro. In particular the					
CC	polypeptides encoded by the Enterococcus faecalis nucleotide sequences					
CC	can be used in vaccines to prevent or attenuate an Enterococcal					
CC	infection.					
XX						
SQ	Sequence 20072 BP; 5846 A; 4288 C; 3266 G; 6628 T; 44 other;					
	Query Match	84.0%;	Score 16.8;	DB 20;	Length 20072;	
	Best Local Similarity	90.0%;	Pred. No. 84;			
	Matches 18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
OY	1 agagatgcccaactgtttt 20 					
Dn	7383 agaaatgcacaaactgcttt 7402					

RESULT 11

AAZ92583

ID AAZ92583 standard; DNA; 43795 BP.

AC AAZ92583;

XX 05-JUN-2000 (first entry)

XX Human DAZ genomic sequence, SEQ ID NO:101.

XX DAZ gene; chromosome Yq; male infertility; sperm count; diagnosis;

XX treatment; gene therapy; ss.

XX Homo sapiens.

XX US6020476-A.

XX 01-FEB-2000.

XX 30-OCT-1996; 96US-0742185.

XX 22-SEP-1994; 94US-0310429.

XX 31-JUL-1996; 96US-0690734.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Hawkins T, Reeve MP, Saxena R, Page DC, Reijo R;

XX WPI; 2000-181393/16.

XX New nucleic acid, useful for diagnosis and treatment of reduced sperm

XX count, is derived from the human DAZ or DAZH genes.

XX Claim 6; Fig 11A-L; 110pp; English.

The invention relates to a family of human genes referred to as the DAZ gene family, and to a functional DAZ homologue, DAZH. Members of the DAZ gene family are clustered in the same region of the Y chromosome. In particular, the invention relates to an isolated DAZ gene (AAZ92499) present in interval 6D and/or 6E of the distal portion of Yq, mutations in which are associated with reduced sperm count. The DAZH gene (AAZ92580) is located on chromosome 3; however, the entire DAZH gene family, including DAZH is expressed in germ cells. DAZ and DAZH nucleotide sequences may be used as a source of primers and probes for the diagnosis of cases of reduced sperm count associated with alteration or deletion of the DAZ gene. They are also used as human chromosome Y markers. Functional DAZ genes can be used in gene therapy for treating reduced sperm counts. Sequence AAZ92499 represents human DAZ cDNA, and sequences AAZ92583-92584 are genomic DAZ sequences. Sequences AAZ92491-92492 are partial DNA sequences of DAZ gene family members.

SQ Sequence 43795 BP; 12175 A; 8166 C; 8183 G; 15271 T; 0 other;

Query Match Best Local Similarity 84.0%; Score 16.8; DB 21; Length 43795;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20

DB 22516 agagatgcccaactgtttt 22535

RESULT 12

AAH41226

ID AAH41226 standard; DNA; 349980 BP.

AC AAH41226;

XX 29-OCT-2001 (first entry)

XX Pyrococcus abyssi genomic fragment #5.

XX Hyperthermophilic archaeon; hyperthermophilic protein; ds.
 XX Pyrococcus abyssi.

XX Key misc-feature Location/Qualifiers

XX misc-feature 1..49980 /tag= a

XX misc-feature 300001..349980 /note= "this sequence overlaps with the 3' end of

XX misc-feature 300001..349980 /tag= b

XX misc-feature 300001..349980 /note= "this sequence overlaps with the 5' end of

XX FR2792651-A1.

XX 27-OCT-2000.

XX 21-APR-1999; 99FR-0005034.

XX 21-APR-1999; 99FR-0005034.

XX (CNRS) CNRS CENT NAT RECH SCI

XX (IFREMER) IFREMER INST FR RECH EXPL MER.

XX Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

XX Querellou J, Weissenbach J, Saurin W, Hellig R;

XX WPI; 2001-126236/14.

XX New nucleotide sequences isolated from Pyrococcus abyssi encode

XX proteins useful in industry.

XX Claim 1; Page 511-606; 1657pp; French.

The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAH41225 and the 3' end of this sequence overlaps with the 5' end of AAH41227. The proteins of the present invention have various potential industrial uses, degrees centrifuge. Note: This patent is in the same patent family as WO2000065062, which contains additional sequences as shown in AAB99132-AAB99143, AAB75903-AAH75920 and AAG66436.

SQ Sequence 349980 BP; 98084 A; 80447 C; 77665 G; 93784 T; 0 other;

Query Match Best Local Similarity 84.0%; Score 16.8; DB 22; Length 349980;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20

DB 53995 aagatgcccaactgtttt 54014

RESULT 13

AAH99123

ID AAH99123 standard; cDNA; 396 BP.

AC AAH99123;

XX 12-OCT-2001 (first entry)

XX Human EST-derived coding sequence SEQ ID NO: 980.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX	01-JUN-2000;	2000MO-US51535.
PF		
XX	11-JUN-1999;	99US-0138632.
XX	(HUMA-)	HUMAN GENOME SCI INC.
PA	(ROSE/)	ROSEN C A.
XX	Rosen CA,	Ruben SM, Komatsoulis GA;
P1		
DR	WPI:	2001-071257/08.
DR	P-PSDB;	AAB75259.
XX		
PT	Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -	
XX		
PS	Claim 1; Page 451; 530pp; English.	
XX		
CC	This invention relates to polynucleotide sequences AAF63789 - AAF63836 which encode human secreted proteins AAB75260 - AAB75287. Included in the invention are protein sequences AAB75288 - AAB75341 which are fragments of the secreted proteins and amino acid sequences with which these fragments share homology. Examples of the activities of the proteins and polynucleotides and the activities of their agonists and antagonists include; immunosuppressive; antiarthritic; antitumoural; antiproliferative; cytostatic; cardiatic; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virocidic; fungicide; optalmalogical; and vulnerary activity. The protein and polynucleotide sequences, their agonists and antagonists may be useful for treating, preventing and diagnosing diseases and disorders such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used in the identification and characterisation of the DNA and protein sequences of the invention.	
CC		
CC	Sequence 1157 BP; 326 A; 223 C; 269 G; 339 T; 0 other;	
SQ		
Query Match	Score 15.8; DB 22; Length 1157;	
Best Local Similarity	89.5%; Pred. No. 1.7e+02;	
Matches 17; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
OY	2 gagatgcccaactgtttt 20 	
Db	138 GAGAA GCCCAAC TCGTTT 120	
RESULT 15		
AAZ49395/C		
ID	AAZ49395 standard; cDNA; 1193 BP.	
XX		
AC	AAZ49395;	
XX		
DT	14-MAR-2000 (first entry)	
XX		
DE	Human STRAP-1 cDNA.	
KM	Serpentine transmembrane antigen of the prostate; sTRAP-1; prostate;	
KM	transmembrane domain; type IIIa membrane protein; expression; cancer;	
KM	prostate cancer; bladder cancer; colon cancer; pancreatic cancer;	
KM	ovarian cancer; tumour antigen; immunisation; immune response;	
KM	cellular; humoral; anticancer vaccine; antibody; detection; diagnosis;	

prognosis; monitoring; susceptibility; therapeutic inhibitor;
drug targeting; recombinant protein; ds.

Homo sapiens.

Location/Qualifiers
64.1083
/tag= a
/product= "Human STRAP-1 (serpentine transmembrane
antigen of the prostate)"

WO9962941-A2.

09-DEC-1999.

01-JUN-1999; 99WO-US12157.

01-JUN-1998; 98US-0087520.
30-JUN-1998; 98US-0091183.

(UROC-) UROGENESYS INC.

(AFAR/) AFAR D E.
(HUBE/) HUBERT R S.
(LEON/) LEONG K.
(RAIT/) RAITANO A B.
(SAFE/) SAFRAN D C.

Afar DE, Hubert RS, Leong K, Raitano AB, Safran DC;
WPI: 2000-072832/06.
P-PSDB; AAY58194.

Novel proteins useful as diagnostic markers and therapeutic targets,
particularly for prostatic cancer

Claim 4; Fig 1A: 83pp; English.

This sequence represents cDNA encoding a novel human protein, STRAP-1 (serpentine transmembrane antigen of the prostate). STRAP-1 is the prototype member of the STRAP family of proteins (AAY58194-Y58197) which exhibit a high degree of structural conservation, but which show no significant structural homology to known human proteins. The STRAP-1 gene has been localised to chromosome 7p22. STRAP-1 is thought to be a type IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 339 amino acid protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. STRAP-1 mRNA and protein expression is maintained at high levels and throughout all stages of prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in certain other cancers, including bladder, colon, pancreatic and ovarian cancer. The function of the STRAP proteins is not known. They may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from immunohistochemical staining). STRAP-1 and STRAP-2 are cell-surface tumour antigens. Immunisation with a STRAP protein induces cellular and humoral immune responses against STRAP-expressing cells. STRAP proteins may be used to identify specific binding agents, to produce anticancer vaccines and to generate specific antibodies. The antibodies may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic inhibitors or to target therapeutic agents to their site of action. STRAP nucleic acids may be used for recombinant protein production, as diagnostic and prognostic reagents, for identifying STRAP-expressing cells for screening inhibitors of STRAP expression and for therapeutic modulation/inhibition of STRAP expression. Since high levels of STRAP proteins are exposed on the cell surface, they are easily targeted by systemically administered agents, and because they are expressed mainly on prostatic epithelial cells, agents targeted to them should have minimal side effects on other tissues.

Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 other;

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 21; Length 1193;
Matches 17; Conservatve 89.5%; Pred. No. 1.7e+02;
0; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagatgccccacgtttt 20
||| ||||| ||||| |||
Db 564 GAGAAAGCCCAACTGCTTT 546

Search completed: September 7, 2002, 18:39:44
Job time: 29878 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:38 ; Search time 12179.2 Seconds
(without alignments)
34.364 Million cell updates/sec

Title: US-09-834-291-1_COPY_44_63
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Genem1:
1: gb_ba:*
2: gb_hhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hhg_hum:*
31: em_hhg_inv:*
32: em_hhg_inv:*
33: em_hhg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

1	20	100.0	20	6	AX026100	Sequence
2	20	100.0	40	6	AX026106	Sequence
3	20	100.0	40	6	AX026114	Sequence
4	20	100.0	2344	6	HSCD955FR	Sequence
5	20	100.0	2827	6	AX026092	Sequence
6	20	100.0	3212	6	AX026089	Sequence
7	20	100.0	187313	9	AL157394	Human DNA
8	18.4	92.0	74951	9	AL151364	Human DNA
9	18.4	92.0	90478	2	AL365355	Homo sapi
10	18.4	92.0	168522	2	AC024302	Homo sapi
11	18.4	92.0	181497	2	AC099561	Homo sapi
12	18.4	92.0	236685	2	AC084744	Mus muscu
13	17.4	87.0	16157	1	AE001670	Chlamydia
14	17.4	87.0	17395	1	AE002255	Chlamydia
15	17.4	87.0	20563	2	AC015202	Drosophila
16	17.4	87.0	121249	5	AL591593	Drosophila
17	17.4	87.0	128969	2	AC018486	Homo sapi
18	17.4	87.0	156136	2	AC079160	Homo sapi
19	17.4	87.0	181053	3	AC022346	Rattus no
20	17.4	87.0	241213	1	AC103322	Rattus no
21	17.4	87.0	325865	1	AP002548	Chlamydia
22	17.4	85.0	34200	8	AB022785	Homo sapi
23	17	85.0	37068	8	AC067938	Neurospor
24	17	85.0	43556	8	AC067937	Neurospor
25	17	85.0	96376	2	AP000065	Homo sapi
26	17	85.0	100000	9	AC084024	Homo sapi
27	17	85.0	134086	2	AC021680	Homo sapi
28	17	85.0	154671	2	AP004461	Oryza sat
29	17	85.0	162925	2	AC091962	Homo sapi
30	17	85.0	196951	2	AL671173	Mus muscu
31	17	85.0	199080	2	AL672345	Mus muscu
32	17	85.0	216188	2	AX026101	Sequence
33	16.8	84.0	661	14	HPV8407	Human Papill
34	16.8	84.0	661	14	HPV8407	Human Papill
35	16.8	84.0	1876	3	AF363304	Bairdiodo
36	16.8	84.0	1876	3	AF363304	Bairdiodo
37	16.8	84.0	3006	9	HSL81913	Human papill
38	16.8	84.0	7537	14	HPV15173	Human papill
39	16.8	84.0	17518	2	AC110307	Rattus no
40	16.8	84.0	28006	2	AC109534	Rattus no
41	16.8	84.0	37906	9	HSU157D4	Human DNA
42	16.8	84.0	42303	9	AL355133	Human DNA
43	16.8	84.0	43795	9	AC000022	Genomic s
44	16.8	84.0	54207	2	AP002024	Homo sapi
45	16.8	84.0	54554	9	AC009500	Homo sapi

ALIGNMENTS

RESULT 1
AX026100 20 bp DNA Linear PAT 16-SEP-2000
Sequence 12 from Patent DE19847779.
AX026100
AX026100.1 GI:10187531

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mueller-Schilling, M., Krammer, P. and Oren, M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 12 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source Location/Qualifiers
1..20
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 6 a 4 c 4 g 6 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 1 AGAGATGCCCAACTGTGTTT 20

RESULT 2
LOCUS AX026106 40 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 18 from Patent DE19847779.
ACCESSION AX026106
VERSION AX026106.1 GI:10187537
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling, M., Krammer, P. and Oren, M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 1984779-C 18 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source location/Qualifiers
1. 40
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 14 a 11 c 5 g 10 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 11 AGAGATGCCCAACTGTGTTT 30

RESULT 3
LOCUS AX026114 40 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 26 from Patent DE19847779.
ACCESSION AX026114
VERSION AX026114.1 GI:10187545
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling, M., Krammer, P. and Oren, M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 1984779-C 26 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source location/Qualifiers
1. 40
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 14 a 11 c 5 g 10 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 11 AGAGATGCCCAACTGTGTTT 30

RESULT 4
LOCUS HSCD955FR 2344 bp DNA linear PRI 05-FEB-1997
DEFINITION H.sapiens CD95 gene 5' flanking region.
ACCESSION X87625
VERSION X87625.1 GI:902311
KEYWORDS beta interferon, CD95 gene, silencer.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2344)
AUTHORS Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and
Watson, V.
TITLE Identification of a silencer, enhancer, and basal promoter region
JOURNAL DNA Cell Biol. 14 (11), 931-937 (1995)
MEDLINE 96069539
REFERENCE 2 (bases 1 to 2344)
AUTHORS Rudert, F.H.
TITLE Direct Submision
JOURNAL Submitted (26-MAY-1995) F.H. Rudert, Genesis Research &
Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
OVERLAPS with X81335, & X82279-X82286.
FEATURES
source location/Qualifiers
1. 2344
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/germline
/tissue-type="Placenta"
/map="q24.1"
564..1337
/note="silencer"
717..801
/note="beta interferon silencer B motifs"
complement(1237..1244)
/note="Lysozyme silencer 1"
1338..1919
1920..2344
/note="Basal promoter"

BASE COUNT 637 a 546 c 511 g 650 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2344;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agagatgcccaactgtttt 20
Db 161 AGAGATGCCCAACTGTGTTT 180

RESULT 5
LOCUS AX026092 2827 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 4 from Patent DE19847779.
ACCESSION AX026092
VERSION AX026092.1 GI:10187523
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2827)
AUTHORS Mueller-Schilling, M., Krammer, P. and Oren, M.

TITLE Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
 JOURNAL Patent: DE 1984779-C 4 03-FEB-2000;
 DEUTSCHES KREBSFORSCH (DE)
 FEATURES Location/Qualifiers
 SOURCE 1..2827
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 728 a 676 c 657 g 766 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2827;
 Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

OY 1 agagatgcccaactgtttt 20
 ||||||||||||||||||
 Db 44 AGAGATGCCCAACTGTTT 63

RESULT 6
 LOCUS AX026089 3212 bp DNA linear PAT 16-SEP-2000
 DEFINITION Sequence 1 from Patent DE1984779.
 ACCESSION AX026089
 VERSION AX026089.1 GI:10187520
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3212)
 AUTHORS Mueller-Schilling, M., Krammer, P. and Oren, M.
 TITLE Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
 JOURNAL DEUTSCHES KREBSFORSCH (DE)
 FEATURES Location/Qualifiers
 SOURCE 1..3212
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 778 a 784 c 809 g 841 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3212;
 Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

OY 1 agagatgcccaactgtttt 20
 ||||||||||||||||||
 Db 44 AGAGATGCCCAACTGTTT 63

RESULT 7
 LOCUS AL157394 187313 bp DNA linear PRI 22-AUG-2001
 DEFINITION Human DNA sequence from clone Rp11-399019 on chromosome 10, complete sequence.
 ACCESSION AL157394
 VERSION AL157394.15 GI:15384622
 KEYWORDS HMG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 187313)
 AUTHORS Blakey, S.
 TITLE Direct Submission
 JOURNAL Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk

COMMENT
 On Aug 31, 2001 this sequence version replaced g1:14161146.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL, Sw, SWISSPROT, Tr, TrEMBL, Wp, WORMPEP. Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>
 Rp11-399019 is from the library RPI-11.2 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/hacpac/home.htm>
 VECTOR: pACE3.6
 This sequence is the entire insert of clone Rp11-399019 The true left end of clone Rp11-496H23 is at 166408 in this sequence. The true right end of clone Rp11-30415 is at 18704 in this sequence.

FEATURES
 SOURCE 1..187313
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="Rp11-399019"
 /clone_1ib="RPI-11.2"
 100119..100156
 /note="Sequence confirmed by AC015461 sequenced by WIBR."
 100157..100198
 /note="Sequence confirmed by WIBR."
 105808..105972
 /note="Sequence confirmed by WIBR."
 105973..105989
 /note="Sequence confirmed by WIBR."
 misc_feature
 misc_feature
 misc_feature
 BASE COUNT 5569 a 36398 c 36888 g 58358 t
 ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 187313;
 Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

OY 1 agagatgcccaactgtttt 20
 ||||||||||||||||||
 Db 142012 AGAGATGCCCAACTGTTT 142031

RESULT 8
 LOCUS AL513364 74951 bp DNA linear PRI 15-NOV-2001
 DEFINITION Human DNA sequence from clone Rp11-480N10 on chromosome 1, complete sequence.
 ACCESSION AL513364
 VERSION AL513364.10 GI:16973038
 KEYWORDS HMG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 74951)
 AUTHORS Almeida, J.
 TITLE Direct Submission

misc_feature /note="assembly_fragment:00064
fragment_chain:1"
21394..37557
/note="assembly_fragment:01038
fragment_chain:1"
37658..54929
/note="assembly_fragment:00052.0"
55030..62839
/note="assembly_fragment:00124"
62940..74511
/note="assembly_fragment:00131.0"
74612..83633
/note="assembly_fragment:00870"
83734..90478
/note="assembly_fragment:01225"
BASF COUNT 27811 a 16881 c 16980 g 28004 t 802 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 2; Length 90478;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 agagatgcccaactgttt 20
Db 43021 AGAATGCCCAACTGTTT 43040

RESULT 10
AC024302/c 168522 bp DNA linear HTG 14-MAR-2000
LOCUS Homo sapiens clone RP11-23123, WORKING DRAFT SEQUENCE, 18 unordered
DEFINITION pieces.
AC024302.2 GI:7239599
VERSION AC024302.2
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 168522)
Birken, B., Linton, L., Nusbaum, C. and Lander, E.
Unpublished
2 (bases 1 to 168522)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,
Bouhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Deatellano, K., Dewar, K., Diaz, J.S., Dodge, S., Dominko, M., Doyle, M.,
Fenster, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hages, B., Heaford, A., Horton, L.,
Howard, J.C., Illey, I., Johnson, R., Lehoczek, J., Levine, R.,
Klein, J., Landers, T., Laroque, K., Lehoucq, P., Marquis, N., McCarthy, M.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McEwan, P., McGurk, A., McKernan, K., McPherson, R., Meldrum, J.,
Meneus, L., Mihova, T., Miranda, C., Mianga, W., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M.,
Peterson, K., Pierre, N., Pisanic, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severyn, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A.,
Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M. Submission

TITLE Direct Submission
JOURNAL Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Mar 14, 2000 this sequence version replaced gi:7108032.
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4376
Center clone name: 23-1-23
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155724 bases at least Q40
Consensus quality: 162423 bases at least Q30
Consensus quality: 164971 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 166822; sum-of-coverage
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-coverage

----- NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1007: contig of 1007 bp in length
* 1008 1107: gap of 100 bp
* 1108 2229: contig of 1122 bp in length
* 2230 2329: gap of 100 bp
* 2330 4120: contig of 1791 bp in length
* 4121 4220: gap of 100 bp
* 4221 6093: contig of 1873 bp in length
* 6094 6193: gap of 100 bp
* 6194 12656: contig of 6463 bp in length
* 12657 12756: gap of 100 bp
* 12757 19311: contig of 6555 bp in length
* 19312 19411: gap of 100 bp
* 19412 24024: contig of 4613 bp in length
* 24025 24124: gap of 100 bp
* 24125 30616: contig of 6492 bp in length
* 30617 30716: gap of 100 bp
* 30717 35830: contig of 5114 bp in length
* 35831 35930: gap of 100 bp
* 35931 45340: contig of 9410 bp in length
* 45341 45440: gap of 100 bp
* 45441 55960: contig of 10520 bp in length
* 55961 56060: gap of 100 bp
* 56061 67711: contig of 11651 bp in length
* 67712 67811: gap of 100 bp
* 67812 78627: contig of 10816 bp in length
* 78628 78727: gap of 100 bp
* 78728 91285: contig of 12558 bp in length
* 91286 91385: gap of 100 bp
* 91386 106039: contig of 14654 bp in length
* 106040 106139: gap of 100 bp
* 106140 123134: contig of 16995 bp in length
* 123135 123234: gap of 100 bp
* 123235 140131: contig of 16897 bp in length
* 140132 140231: gap of 100 bp
* 140232 168522: contig of 28291 bp in length.
Location/Qualifiers
1. 168522
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RP11-23123"
/clone_lib="RP11-23123"
1. 1007
/note="assembly_fragment"
1108..2229
/note="assembly_fragment"

FEATURES
SOURCE
misc_feature
misc_feature
misc_feature

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misc_feature      2330..4120
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misc_feature      4221..6093
                  /note="assembly_fragment"
misc_feature      6194..12656
                  /note="assembly_fragment"
misc_feature      12757..19311
                  /note="assembly_fragment"
misc_feature      19412..24024
                  /note="assembly_fragment"
misc_feature      24125..30616
                  /note="assembly_fragment"
misc_feature      30717..35830
                  /note="assembly_fragment"
misc_feature      35931..45340
                  /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                  clone_end:SP6
vector_side:right"
45441..55960
/note="assembly_fragment"
56061..67711
/note="assembly_fragment"
67812..78627
/note="assembly_fragment"
vector_side:left"
78728..91285
/note="assembly_fragment"
91386..106039
/note="assembly_fragment"
106140..123134
/note="assembly_fragment"
123235..140131
/note="assembly_fragment"
140232..168522
/note="assembly_fragment"
BASE COUNT      54289 a 31221 c 31549 g 49758 t 1705 others
ORIGIN

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Query Match      92.0% Score 18.4; DB 2; Length 168522;
Best Local Similarity 95.0% Pred. No. 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 agagatgcccaactgtttt 20
    ||| ||||| ||||| |||||
Db 145086 AGAATGCCCAACTGTTT 145067

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RESULT 11
AC099561      181497 bp DNA linear HTG 16-NOV-2001
DEFINITION    Homo sapiens chromosome 1 clone RP11-193H16, WORKING DRAFT
ACCESSION     AC099561 AC1356153
VERSION       AC099561.1 GI:16945998
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVERFIN.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      1 (bases 1 to 181497)
TITLE         Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
JOURNAL       Direct Submission
REFERENCE     2 (bases 1 to 181497)
AUTHORS      Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE         Direct Submission
JOURNAL       Submitted (16-NOV-2001) Genome Center, University of Washington,
COMMENT       Box 352145, Seattle, WA 98195, USA
              On Nov 16, 2001 this sequence version replaced gi:12331033.
              ----- Genome Center
              Center: University of Washington Genome Center

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Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
Drafting Center: SC
----- Project Information
Center project name: chr-1
Center clone name: RP11-193H16 (sc0121)
----- Summary Statistics
Sequencing vector: plasmid; 108752; 90% of reads
Sequencing vector: plasmid; 10% of reads
Chemistry: Dye-terminator ET; 73% of reads
Chemistry: Dye-terminator Big Dye; 27% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178264 bases at least Q40
Consensus quality: 179524 bases at least Q30
Insert size: 169266; 11.4% error; agarose-fp
Insert size: 180697; sum-of-contigs
Quality coverage: 8.9x in Q20 bases; agarose-fp
Quality coverage: 8.4x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 2355: contig of 2355 bp in length
* 2356: gap of unknown length
* 2456: gap of unknown length
* 4495: contig of 2040 bp in length
* 4496: gap of unknown length
* 4596: gap of unknown length
* 7640: contig of 3045 bp in length
* 7641: gap of unknown length
* 7741: 12425: contig of 4685 bp in length
* 12426: gap of unknown length
* 12525: gap of unknown length
* 12526: 17171: contig of 4646 bp in length
* 17172: 17271: gap of unknown length
* 17272: 26889: contig of 9618 bp in length
* 26890: 26989: gap of unknown length
* 26990: 62181: contig of 35192 bp in length
* 62182: 62281: gap of unknown length
* 62282: 109708: contig of 47421 bp in length
* 109709: 109808: gap of unknown length
* 109809: 181497: contig of 71689 bp in length.
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Location/Qualifiers
1. 181497
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-193H16"
/clone_lib="RPCT human BAC library 11"
1. 2355
/note="assembly_name:Contig96"
2456..4495
/note="assembly_name:Contig99"
4596..7640
/note="assembly_name:Contig102"
7741..12425
/note="assembly_name:Contig101"
12526..17171
/note="assembly_name:Contig103"
17272..26889
/note="assembly_name:Contig104"
26990..62181
/note="assembly_name:Contig105"
62282..109708
/note="assembly_name:Contig106"
109809..181497
/note="assembly_name:Contig107"
BASE COUNT      58138 a 34626 c 32770 g 55026 t 937 others
ORIGIN

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[illegible]

FEATURES	source	Location/Qualifiers
BASE COUNT	58998 a 57976 c 57568 g 58324 t 3819 others	
ORIGIN	/organism="Mus musculus" /db_xref="taxon:10090" /clone="RP23-15A13"	
Query Match	92.0%; Score 18.4; DB 2; Length 236685;	
Best Local Similarity	95.0%; Pred. No. 20;	
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
OY 1 agagatgcccaactgtttt 20		
DB 236285 AGAAATGCCCAACTGTTTT 236266		
RESULT 13		
AE001670/c	16157 bp	DNA linear BCT 01-DEC-2000
AE001670		

DEFINITION Chlamydia pneumoniae section 86 of 103 of the complete genome.
ACCESSION AE001670 AE001363
VERSION AE001670.1 GI:4377212
KEYWORDS Chlamydia pneumoniae CWL029.
SOURCE Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
ORGANISM
REFERENCE
AUTHORS Kaiman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,
1 (bases 1 to 16157)
Olinger, L., Grimwood, J., Davis, R. W., and Stephens, R. S.,
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
JOURNAL Nat. Genet. 21 (4), 385-389 (1999)
MEDLINE 99206606
PUBMED 10192388
REFERENCE
AUTHORS 2 (bases 1 to 16157)
Kaiman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,
Grimwood, J., Davis, R. W., and Stephens, R. S.,
Direct Submission
JOURNAL Submitted (01-DEC-1998) Program in Infectious Diseases, University
of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
FEATURES
source
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/strain="CWL029"
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NEKLVHTDFSGRNKYGVRERGMATINNGSLAYSOVRRPGGRTVIFSDYMRATILA
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QY 2 gagatgcccaaacgtttt 20
Db 4110 GAGATGCCCAAACTGTTT 4128

RESULT 15
AC015202
LOCUS
DEFINITION
AC015202 20563 bp DNA linear HTG 16-NOV-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
AC015202
VERSION AC015202.1 GI:6436133
KEYWORDS HTG; HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 20563)
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,

COMMENT

Rockville, MD, USA
This sequence was identified as CDM:10213741 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES

source

1. .20563

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

6416 a 4099 c 4148 g 5900 t

BASE COUNT

6416 a 4099 c 4148 g 5900 t

ORIGIN

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Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 agagatgcccactgttt 19

Db 2966 AGAGATGCCCAACTGATT 2984

Search completed: September 7, 2002, 18:21:55
Job time: 28814 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:20 ; Search time 8462.63 seconds
(without alignments)
191.387 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456
Perfect score: 120
Sequence: 1 taagggaaggggtatggca.....aatgttgcttaagctttttt 120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	43.2	36.0	716	10 BG256799	BG256799 602371024
2	42.4	35.3	488	12 AG019885	AG019885 Homo sapi
3	42.4	35.3	756	12 AG019562	AG019562 Homo sapi
4	40.6	33.8	469	9 AA279976	AA279976 zt08e01.s
5	40.2	33.5	421	12 AG033226	AG033226 HS_2226.A
6	39.9	32.5	698	12 AG093829	AG093829 Pan trogl
7	38.8	32.3	530	12 AG070826	AG070826 HS_5571_A
8	38.8	31.7	691	12 AG040694	AG040694 CIT-HSP-2
9	37.4	31.2	367	9 AA376998	AA376998 EST89574
10	37.4	31.2	437	12 AG049848	AG049848 HS_5088_B
11	36.8	30.7	605	12 AG054706	AG054706 CIT-HSP-2
12	36.6	30.5	686	12 AG259094	AG259094 1M0400K14
13	35.8	29.8	482	12 AG060369	AG060369 HS_2126.A
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15	35.8	29.8	719	12 AG089826	AG089826 HS_3100_A
16	35.8	29.8	750	12 AG089007	AG089007 HS_3100_A
17	35.6	29.7	497	12 AG375661	AG375661 RPI11-15

C 18	35.6	29.7	590	12	AQ375699	AQ375699 RPI11-15
C 19	35.6	29.7	718	12	AQ108019	AQ108019 CIT-HSP-2
C 20	35.2	29.3	220	9	AW903211	AW903211 CM4-NN102
C 21	35.2	29.3	268	10	C17241	C17241 C17241 Clon
C 22	35.2	29.3	270	10	C16982	C16982 C16982 Clon
C 23	35.2	29.3	301	9	AA350574	AA350574 EST57929
C 24	35.2	29.3	346	9	AV694681	AV694681 AV694681
C 25	35.2	29.3	353	9	AA362251	AA362251 EST71725
C 26	35.2	29.3	377	9	AV692265	AV692265 AV692265
C 27	35.2	29.3	394	10	BG897243	BG897243 HOA60-1-H
C 28	35.2	29.3	474	12	AQ146371	AQ146371 HS_2228_A
C 29	35.2	29.3	688	12	AQ420313	AQ420313 RPI1-11-1
C 30	35.2	29.3	740	12	AQ420267	AQ420267 RPI1-11-1
C 31	35	29.2	444	12	B35593	B35593 HS-1029-A2-
C 32	35	29.2	448	12	B36994	B36994 HS-1042-A2-
C 33	35	29.2	585	12	AQ056850	AQ056850 HS_5338_B
C 34	35	29.2	642	12	AG125770	AG125770 Pan trogl
C 35	35	29.2	387	12	AG011233	AG011233 HS_3239_B
C 36	34.8	29.0	399	10	BG011412	BG011412 RCI-GN026
C 37	34.8	29.0	497	12	B39893	B39893 HS-1050-B1-
C 38	34.8	29.0	527	9	AW297626	AW297626 UT-H-BMO-
C 39	34.8	29.0	696	12	B10814	B10814 F18A15-SP6
C 40	34.6	28.8	384	9	AV743395	AV743395 AV743395
C 41	34.6	28.8	397	9	A1244275	A1244275 g181b01.x
C 42	34.6	28.8	414	9	A1469365	A1469365 t171c12.x
C 43	34.6	28.8	429	12	AQ170644	AQ170644 HS_2165_A
C 44	34.6	28.8	441	12	B95491	B95491 CIT-HSP-216
C 45	34.6	28.8	466	9	A1635956	A1635956 tz28e11.x

ALIGNMENTS

RESULT 1
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LOCUS 602371024F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4479221 5',
DEFINITION mRNA sequence.
ACCESSION BG256799.1 GI:12766615
VERSION BG256799.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 716)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@rsf@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LLM10310 row: p column: 06
High quality sequence stop: 708.
Location/Qualifiers
1. 716
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Site: 2; Salt; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH-MGC Library."

FEATURES

source

BASE COUNT	193 a	133 c	142 g	248 t
ORIGIN				
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QY	84	aactaacatcttggccaatgttgccttaagctctttt 119		
Db	336	AGTCATGTGGCCTTGCTGTAFTTACTTAACTTTCT 371		
RESULT	2		488 bp	DNA
AG019885/c				linear
LOCUS	AG019885			GSS 16-OCT-1999
DEFINITION	Homo sapiens genomic DNA, 21q region, clone: B2289H10 X094 (RP),			
ACCESSION	AG019885			
VERSION	AG019885.1			
KEYWORDS	GI:6045829			
SOURCE	GSS.			
ORGANISM	Homo sapiens DNA, clone:B2289H10 X094 (RP).			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 488)			
TITLE	Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T., Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.			
JOURNAL	Homo sapiens genomic DNA, chromosome 21q			
REFERENCE	Published Only in Database (1999) In press			
AUTHORS	2 (bases 1 to 488)			
TITLE	Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T., Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.			
JOURNAL	Direct Submission			
FEATURES	Submitted (16-OCT-1999) to the DDBJ/EMBL/GenBank databases.			
Source	Submitted Hattori, RIKEN Genomic Sciences Center(GSC) c/o Kitasato University; 1-15-1 Kitasato, Sagamihara 228-8555, Japan (E-mail:hattori@hgsc.ims.u-tokyo.ac.jp, Tel:042-778-9923, Fax:042-778-9924)			
Location/Qualifiers	1..488			
BASE COUNT	144 a	95 c	107 g	142 t
ORIGIN				
Query Match	35.3%;	Score 42.4;	DB 12;	Length 488;
Best Local Similarity	62.0%;	Pred. No. 0.029;		
Matches	67;	Conservative	0;	Mismatches 41; Indels 0; Gaps 0;
QY	12	ggatgagcatagaagaagcagcagccttggggagcagaatatcatgaattcctgaact 71		
Db	481	GGTATCATGAGAACACACCAAACTCACTGAGTCAGACAGAACCTGGGTTTGATCCTGACT 422		
QY	72	ctgcattattataacacacatccttggccaatgttgccttaagctttt 119		
Db	421	CTGCTATTCTTAACTGCTGTCACACCTGGGAAATAATTACTTTTCT 374		
RESULT	3		756 bp	DNA
LOCUS	AG019562/c			linear
DEFINITION	Homo sapiens genomic DNA, 21q region, clone: B2289H10 A011(-21),			
ACCESSION	AG019562			

```

VERSION      AG019562.1  GI:6045506
KEYWORDS
SOURCE       Homo sapiens DNA, clone:B2289H10 A011(-21).
ORGANISM     Homo sapiens
REFERENCE    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE        Hattori.M., Fujiyama.A., Ishii.K., Toyoda.A., Taylor.T.,
REFERENCE    Park.H.-S., Yada.T., Watanabe.H. and Sakaki.Y.
AUTHORS      Homo sapiens genomic DNA, chromosome 21q
TITLE        Published Only in Database (1999) In press
REFERENCE    2 (bases 1 to 756)
AUTHORS      Hattori.M., Fujiyama.A., Ishii.K., Toyoda.A., Taylor.T.,
TITLE        Park.H.-S., Yada.T., Watanabe.H. and Sakaki.Y.
JOURNAL      Submitted (16-OCT-1999) to the DDBJ/EMBL/GenBank databases.
REFERENCE    Masahira Hattori, RIKEN Genomic Sciences Center(GSC) c/o Kitasato
AUTHORS      University; 1-15-1 Kitasato, Sagamihara 228-8555, Japan
TITLE        (E-mail:hattori@hgsc.ims.u-tokyo.ac.jp; Tel:042-778-9923,
JOURNAL      Fax:042-778-9924)
FEATURES
source       Location/Qualifiers
             1..756
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /chromosome="21"
             /clone="B2289H10 A011(-21)"
             /map="21q"
BASE COUNT   240 a 135 c 140 g 241 t
ORIGIN
Query Match 35.3%; Score 42.4; DB 12; length 756;
Best Local Similarity 62.0%; Pred. No. 0.031;
Matches 67; Conservative 0; Mismatches 41; Indels 0; Gaps 0
QY 12 ggatgagcctaaagagcagcagccttggcgagcaagaatactaaagttaacttcgact 71
Db 430 ggatcattcgtatgacacgacacaaagctactggaactcgagacacacctgggttggaatcctgact 371
QY 72 ctgcctatttatttaactaacacatccttgcgcaagtgcgttaagctttt 119
Db 370 ctgctatttcttttagctgtgcacacctgggaaatttagtttaacttttct 323
RESULT 4
LOCUS       AA279976 469 bp mRNA linear EST 15-AUG-1997
DEFINITION  zt08e01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712536 3',
ACCESSION   AA279976
VERSION     AA279976
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE       1 (bases 1 to 469)
NCI_CGAP    http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL     Tumor Gene Index
COMMENT     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 717 Std Error: 0.00
Seq primer: -41m13 fwd. RT from Amerham
High quality sequence stop: 398.
Location/Qualifiers
1..469
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:712536"
FEATURES
source

```

BASE COUNT	143 a	85 c	58 g	129 t	6 others
ORIGIN					
Query Match		33.5%;	Score 40.2;	DB 12;	Length 421;
Best Local Similarity		63.2%;	Pred. No. 0.12;	35;	Indels 0; Gaps 0;
Matches	60;	Conservative	0;	Mismatches	0;
QY	25	aagagcagacccttggagcagaagatatcctcaagtttaattcctcgtactcgtcatttata 84			
DB	202	AAGACTATGACCTCTGTGAAGCCAAACCAACTAAACATGAATCTGCTCTGTACATACATA 261			
QY	85	actaacatcttgcacatgttgccttaagctttt 119			
DB	262	ACTTCAGACCCCTTGCGCAAGTTATTTATGTTTNT 296			
RESULT	6				
LOCUS	AG093829	698 bp	DNA	linear	GSS 03-NOV-2001
DEFINITION	Pan troglodytes DNA, clone: PTB-094G15.F, genomic survey sequence.				
ACCESSION	AG093829				
VERSION	AG093829.1	GI:16645631			
KEYWORDS	GSS; GSS (genome survey sequence).				
SOURCE	Pan troglodytes male lymphoblast DNA, clone: lib:PTB Chimpanzee Male BAC library clone: PTB-094G15.F.				
ORGANISM	Pan troglodytes				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.				
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.				
TITLE	BAC end sequences of library PTB				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 698)				
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suheiho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
COMMENT	1-E-mail: schimpes@gscc.riken.go.jp, URL: http://hnp.gscc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)				
COMMENT	Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the Rad process and may have higher chance of clone tracking errors.				
PRIMERS	Sequencing: -21M13				
LIBRARY	Vector : PKS145				
R.Site 1	: SacI				
R.Site 2	: SacI				
Location/Qualifiers					
1. 698					
/organism="Pan troglodytes"					
/db_xref="taxon:9598"					
/clone="PTB-094G15.F"					
/sex="male"					
/cell_type="lymphoblast"					
/clone_lib="PTB Chimpanzee Male BAC Library"					
BASE COUNT	197 a	165 c	134 g	198 t	4 others
ORIGIN					
Query Match		32.5%;	Score 39;	DB 12;	Length 698;
Best Local Similarity		63.2%;	Pred. No. 0.3;		
Matches	60;	Conservative	0;	Mismatches	35; Indels 0; Gaps 0;
QY	25	aagagcagacccttggagcagaagatatcctcaagtttaattcctcgtactcgtcatttata 84			
DB	180	AAAAGCCAGACTTTGAAGCCAGACTGCTTGAAGTCAAACTGCTGCTGCGCAGTTATTA 239			
QY	85	actaacatcttgcacatgttgccttaagctttt 119			

Db 240 GTTATATGACCTTGAGCATAATTACTTAACCTCTCT 274

RESULT	7
A0708262	
LOCUS	530 bp DNA linear GSS-07-JUL-1993
DEFINITION	H5_5571_A1.F11.T7A RPCI-II Human Male BAC Library Homo sapiens
ACCESSION	A0708262
VERSION	A0708262.1 GI:5417688
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	Mammalia: Chordata; Chordata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 530)
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace TG, Hood L

or from Resear h Genetics (info@resgen.com). BAC end web Server:
<http://www.htsc.washington.edu>
 Plate: 1147 row: K column: 21
 Seq primer: r7
 Class: BAC ends
 High quality sequence stop: 530.
 Location/Qualifiers
 1..530

DEFINITION	CIT-HSP-2386K22..TF.1 CIT-HSP Homo sapiens genomic clone 2386K22.
ACCESSION	DNA sequence.
VERSION	AQ240694
KEYWORDS	AQ240694.1 GI:3672892
KEYWORDS	GSS.

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Human.	Homo sapiens			Use of a random human BAC End Sequence Database for Sequence-Real		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				Map Building		
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				unpublished (1998)		
1 (bases 1 to 691)				Other csses. Ctm-hfn-2266722 and 1		
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K						
Berry,K.K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and						
Venter,J.C.						

FEATURES	SOURCE	Location/Qualifiers
1. .691		
/organism="Homo sapiens"		
/db_xref="taxon:9606"		
/clone="238K22"		
/clone_lib="CIR-HSP"		
/sex="Male"		
/cell_type="Sperm"		
/note="Vector: pBeloBAC11; site_1: HindIII; site_2: HindIII"		
263 a	99 c	103 g 225 t 1 others

EST	LOCUS	EST	LINEAR	EST
9				21-APR-1998
AA376998				
AA376998		367 bp	MRNA	
AA376998				
EST895574	Small intestine			
AA376998				
AA376998.1	GI:2029388			
EST.				
human.				

HOMO SAPIENS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 I (bases 1 to 367)
 Adams,M.D., Keilavage,A.R., Fleischmann,R.D., Fullmer,R.A., Bult
 C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.C., Gocayne,J.D., White
 O., Sutton,G., Blake,J.A., Brandon,R.C., Mar-Wal,C., Clayton,R.A.,
 Cline,T.R., Cotton,M.D., Eaker-Hughes,J., Fine,L.D., Fitzgerald
 L.M., Fitzhugh,W.M., Fitchman,J.T., Geoghegan,N.S., Glodok,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudé,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Peng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., He,W.W., Hu,C.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungnig,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

COMMENT

Contact: Kerlavage, AR

Bioinformatics for Genomic Research

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..367

/organism="Homo sapiens"

/db_xref="ATCC (inhost):181474"

/db_xref="taxon:9606"

/clone_lib="Small intestine I"

/dev_stage="adult"

/note="Organ: small intestine; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

Site_1: EcoRI; Site_2: XhoI

BASE COUNT 110 a 58 c 64 g 134 t 1 others

ORIGIN

Query Match 31.2%; Score 37.4; DB 9; length 367;

Best local Similarity 74.6%; Pred. No. 0.79; Index 0; Gaps 0;

Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 25 aagagcagccttgagcagaatactgaattactctgactctgattatla 84

Db 77 AAAGCCTGAACTTAGAGTAAATACTAGCTTAAAGTCTGCTCTATATTA 136

QY 85 act 87

Db 137 ACT 139

RESULT 10

AQ498448 437 bp DNA linear GSS 28-APR-1999

LOCUS HS.5088.B1.F12.SP6E.RPCT-11 Human Male BAC Library Homo sapiens

DEFINITION genomic clone Plate-664 COL-23 Row=L, DNA sequence.

ACCESSION AQ498448

VERSION AQ498448.1 GI:4698571

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 437)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

MEDLINE 99380589

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end web Server: <http://www.hnsc.washington.edu>

Plate: 664 row: L column: 23

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 437.

Location/Qualifiers

1..437

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-664 COL-23 Row=L"

/clone_lib="RPCT-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

pBACe3.6 vector at EcoRI sites"

BASE COUNT 138 a 72 c 71 g 155 t 1 others

ORIGIN

Query Match 31.2%; Score 37.4; DB 12; length 437;

Best local Similarity 74.6%; Pred. No. 0.81; Index 0; Gaps 0;

Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 25 aagagcagccttgagcagaatactgaattactctgactctgattatla 84

Db 96 AAAGCCTGAACTTAGAGTAAATACTAGCTTAAAGTCTGCTCTATATTA 155

QY 85 act 87

Db 156 ACT 158

RESULT 11

AQ054706 605 bp DNA linear GSS 30-JUL-1998

LOCUS CIT-HSP-2343H11.TF CIT-HSP Homo sapiens genomic clone 2343H11, DNA sequence.

DEFINITION CIT-HSP-2343H11.TF CIT-HSP Homo sapiens genomic clone 2343H11, DNA sequence.

ACCESSION AQ054706

VERSION AQ054706.1 GI:3351312

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 605)

Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Building of a random BAC End Sequence Database for Sequence-Ready Map Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Unpublished (1998)

Other GSSs: CIT-HSP-2343H11.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

```

/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUC1M0400K14"
/clone_1fb="Mouse 10Kb
/sex="Male"
/plasmid UUC1M1 library

```

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FEATURES
Source      Location/Qualifiers
1. .482
/organism="Homo sapiens"

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Search completed: September 7, 2002, 14:51:24
Job time: 16183 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2002, 01:09:18 ; Search time 1826.34 Seconds
(without alignments)
200.099 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456
Perfect score: 120
Sequence: 1 tagggggaagggtatgca.....aatgttgcttaagctttttt 120

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2036664 seqs, 1522705736 residues

Total number of hits satisfying chosen parameters: 4073328

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	45121	6	US-10-035-832-1262
2	38	31.7	633	7	US-10-027-632-281585
3	36.4	30.3	860	7	US-10-027-632-129548
4	36.2	30.2	637	7	US-10-027-632-248649
5	35.8	29.8	471	7	US-10-027-632-295053
6	35.8	29.8	595	7	US-10-027-632-57014
7	35.8	29.8	604	7	US-10-027-632-4265
8	35.8	29.8	604	7	US-10-027-632-4266
9	35.8	29.8	13046	7	US-10-125-340-595
10	35.6	29.7	657	7	US-10-027-632-265257
11	35.4	29.5	162450	5	US-09-345-882-1
12	35.4	29.5	162450	5	US-09-345-882-1
13	35.4	29.5	162450	7	US-10-126-704-1
14	35.2	29.3	606	7	US-10-027-632-231146
15	35.2	29.3	7379	5	US-09-984-827-14
16	35	29.2	825	7	US-10-027-632-167773
17	35	29.2	825	7	US-10-027-632-167774
18	35	29.2	834	7	US-10-027-632-152436
19	35	29.2	834	7	US-10-027-632-152437
20	35	29.2	834	7	US-10-027-632-152438
21	35	29.2	240000	1	PCT-US02-17382-31
22	34.8	29.0	448	5	US-09-918-995-14451
23	34.8	29.0	611	7	US-10-027-632-163012
24	34.8	29.0	611	7	US-10-027-632-174901
25	34.8	29.0	620	6	US-10-198-846-4515

C 26	34.8	29.0	17597	6	US-10-206-664-2409	Sequence 2409, Ap
C 27	34.8	29.0	17597	6	US-10-212-054-2144	Sequence 2144, Ap
C 28	34.8	29.0	378361	1	PCT-US02-21669-3	Sequence 3, Appl
C 29	34.6	28.8	456	5	US-09-918-995-12552	Sequence 12552, A
C 30	34.6	28.8	467	5	US-09-918-995-10146	Sequence 10146, A
C 31	34.6	28.8	496	7	US-10-027-632-333053	Sequence 333053, A
C 32	34.4	28.7	663	7	US-10-137-757-619	Sequence 619, App
C 33	34.4	28.7	2281	7	US-10-027-632-102247	Sequence 102247, A
C 34	34.4	28.7	2281	7	US-10-027-632-102248	Sequence 102248, A
C 35	34.4	28.7	6803	7	PCT-US02-25766-1885	Sequence 1885, Ap
C 36	34.2	28.5	277	6	US-10-198-846-12340	Sequence 12340, A
C 37	34.2	28.5	603	7	US-10-027-632-185527	Sequence 185527, A
C 38	34.2	28.5	1335	7	US-10-126-103-273	Sequence 177, App
C 39	34.2	28.5	25550	7	US-10-105-298-14994	Sequence 14994, A
C 40	34	28.3	619	7	US-10-027-632-277529	Sequence 277529, A
C 41	33.8	28.2	519	7	US-10-027-632-185527	Sequence 185527, A
C 42	33.8	28.2	623	7	US-10-027-632-190488	Sequence 190488, A
C 43	33.8	28.2	623	7	US-10-027-632-190489	Sequence 190489, A
C 44	33.8	28.2	623	7	US-10-027-632-190490	Sequence 190490, A
C 45	33.8	28.2	1029	7	US-10-027-632-30428	Sequence 30428, A

ALIGNMENTS

```
RESULT 1
US-10-035-832-1262
; Sequence 1262, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Engelhard, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1262
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-832-1262

Query Match      100.0%; Score 120; DB 6; Length 45121;
Best Local Similarity 100.0%; Pred. No. 2.7e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taggggaagggtatgcatagaagcagcacttggtggaagaatattagttt 60
    |||||||
Db 8330 taggggaagggtatgcatagaagcagcacttggtggaagaatattagttt 8389
    |||||||

QY 61 aattccgacttgccttatattacacacatcttgcacatgtgttaagctttt 120
    |||||||
Db 8390 aattccgacttgccttatattacacacatcttgcacatgtgttaagctttt 8449
    |||||||

RESULT 2
US-10-027-632-281585/c
; Sequence 281585, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
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? PRIOR APPLICATION NUMBER: US 60/198,676
? PRIOR FILING DATE: 2000-04-20
? PRIOR APPLICATION NUMBER: US 60/193,483
? PRIOR FILING DATE: 2000-03-29
? PRIOR APPLICATION NUMBER: US 60/185,218
? PRIOR FILING DATE: 2000-02-24
? PRIOR APPLICATION NUMBER: US 60/167,363
? PRIOR FILING DATE: 1999-11-23
? PRIOR APPLICATION NUMBER: US 60/156,358
? PRIOR FILING DATE: 1999-09-28
? PRIOR APPLICATION NUMBER: US 60/146,002
? PRIOR FILING DATE: 1999-08-09
? NUMBER OF SEO ID NOS: 325720
? SOFTWARE: FastSEO for Windows Version 4.0
? SEO ID NO 281585
? LENGTH: 633
? TYPE: DNA
? ORGANISM: Human
US-10-027-632-281585

```

	Query Match	31.7%	Score 38	DB 7	Length 633
Best Local Similarity	66.2%	Pred. No.	0.075		
Matches	53	Conservative	1	Mismatches	26
				Indels	0
				Gaps	0
QY	40	ggagcaagaatcctaacttaattcaatcgactgcgtactatttataactaacacattctgc	99		
Db	332	GGAGCAACACATTTGGGTTCAATACCTTAATTCACCAATTACTAGCTGTTTAACCTTGG	273		
QY	100	caatgctgaactaagctttt	119		
Db	272	ACAGGTTTCCTTAACCTCTCT	253		

```

RESULT      3
US-10-027-632-129548
Sequence 129548, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/198,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
PRIORITY FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 129548
LENGTH: 860
TYPE: DNA
ORGANISM: Human
US-10-027-632-129548

```

Query Match	30.3%	Score 36.4	DB 7	Length 860
Best Local Similarity	61.7%	Pred. NO. 0.23		
Matches 58	Conservative	0	Mismatches 36	Indels 0
Gaps 0				

23 gaagagcagacttggagccaagaatacttaattcctgactgcgtattat 82

||||||| || ||||| ||| || || ||||| || || ||||| || |||||

Db 456 gtaagacgcagggaatttttgagtgtagagatgctcgaatttgaatttttaccctgthgatt 555

Q7 83 taactaaccatccttgcgaatggtcctaagctt 116
||||| |
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Db 556 taaccatgtagccttgagtgacgttaacttaacct 559

```

RESULT      4
US-10-027-632-248649
; Sequence 248649, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;   OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 248649
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-248649

```

Query Match	30.2%	Score 36.2	DB 7	Length 637
Best Local Similarity	59.0%	Pred. No. 0.26		
Matches	62	Conservative	0	Mismatches 43; Indels 0; Gaps 0;
QY	15	atggatagaagacgagacctgtggaggaagaatatcaagtttaattcctgactctg	74	
Db	98	atgcgaatataaagatagaagcaactgtggagccaagattccaaqttttaatgcaactt	157	
QY	75	ctatttataactaacacactcttggccaatgtrgtcgaactttt	119	
Db	158	caatttcttaagatctgtgaccttggttccaagtttcttaagcttctc	202	

```

RESULT      5
US-10-027-632-295053/c
: Sequence 295053, Application US/10027632
: GENERAL INFORMATION:
:   APPLICANT: Wang, David G.
:   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
:   POLYMORPHISMS IN THE HUMAN GENOME
:   FILE REFERENCE: 108827.129
:   CURRENT APPLICATION NUMBER: US/10/027,632
:   CURRENT FILING DATE: 2002-04-30
:   PRIOR APPLICATION NUMBER: US 60/218,006
:   PRIOR FILING DATE: 2000-07-12
:   PRIOR APPLICATION NUMBER: US 60/198,676
:   PRIOR FILING DATE: 2000-04-20
:   PRIOR APPLICATION NUMBER: US 60/193,483
:   PRIOR FILING DATE: 2000-03-29
:   PRIOR APPLICATION NUMBER: US 60/185,218
:   PRIOR FILING DATE: 2000-02-24
:   PRIOR APPLICATION NUMBER: US 60/167,363
:   PRIOR FILING DATE: 1999-11-23

```



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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-4266

```

Query Match	29.8%	Score	35.8	DB	7	Length	604
Best Local Similarity	61.1%	Pred. NO.	0.34				
Matches	58	Conservative	0	Mismatches	37	Indels	0
						Gaps	0

```
QY      25 aaagcagcaccttgggacgaataatctaagttaattccgtactctgcattatta   84
         ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db     325 AAGACATGAACCTCGAAGCCAGCACTGTCTATGTCGAATCCCAACTTCATTCTTACA   26
```

QY 85 aciaaccacatttgcacatgttgccttaagctttt 119
 ||| | ||| | | ||||| | | |
 Db 265 GCTACATGACCTTGGACAATACTTAACCTCTCT 231

RESULT 9
US-10-125-540-595/c
: Sequence 595. Application US/10125540

```

: GENERAL INFORMATION:
:
: APPLICANT: Rosen et al.
:
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
:
: FILE REFERENCE: PT214C1

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```

; LENGTH: 13046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-595

```

Query Match	29.8%;	Score 35.8;	DB 7;	Length 13046;
Best Local Similarity	61.1%;	Pred. No. 0.7;		
Matches 58; Conservative	0;	Mismatches 37;	Indels 0;	Gaps 0

DQ 25 aaagacgagcaaccttgggaagcaagaatatccaaatttaattccctactcgtattatata 84
|| ||| | || ||| | || ||| | || ||| | || ||| | || ||| |
Db 8107 AAAAGCAGCACTCTGGAACCAACTGTGTGATTTGATCCCFAGCTCTGCCAATTACTA 8048

Qy	85	actaaccatcttgcgaatgttgcctaagctttt	119
Db	8047	ACTGTGTGACCTTGGGCAAGTTACTTAAGCTTCTCT	8013

RESULT 10
US-10-027-632-265257

GENERAL INFORMATION:

```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILING DATE: 10/08/2001
; FILING OFFICE: 10/08/2001

```

CURRENT FILING DATE: 2003-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

[illegible]

```
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 265257
```

```

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-265257

```

Query Match	29.7%	Score 35.6	DB 7	Length 657
Best local Similarity	71.2%	Pred. NO. 0.4		
Matches 47	Conservative	0	Mismatches 19	Indels 0
				Gaps 0

QY 23 gaaagagcagcagccttgggaggaagaatatctaatcttccgactcgcgtattat 82
 ||||| | | | | | ||||| ||| ||| | |||
 Db 368 gaaagacacagcgtctgttaaccaggtaaatctaatcttcaatccctgcctcgtattcttat 427

QY	83	taacta	88
Db	428	taacta	433

```

RESULT 11
US-09-345-882-1
; Sequence 1, Application US/09345882
; GENERAL INFORMATION:

```

1 TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP)
 2 TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
 3 FILE REFERENCE: GENSET .031A

; CURRENT FILING DATE: 1999-06-30
 ; PRIOR APPLICATION NUMBER: US 60/091,315
 ; PRIOR FILING DATE: 1998-06-30

```
;; PRIOR FILING DATE: 1998-12-10
;; NUMBER OF SEQ ID NOS: 140
;; SOFTWARE: Patent .pm
;; seq id no: 1
```

```

; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

```

NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:

```

```

NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:

```

```

; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:

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```

NAME/NEI:  allele
LOCATION:  93714
OTHER INFORMATION:  5-128-60      :  polymorphic base deletion of GT
FEATURE:

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NAME/NOI : 8181E
LOCATION : 97122
OTHER INFORMATION : 99-1442-224 : polymorphic base G or T
FEATURE:

```

LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:

```

; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G

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; FEATURE:
; NAME/KEY: allele
;

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LOCATION: 99117 : polymorphic base A or G
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE: NAME/KEY: allele
LOCATION: 103806 : polymorphic base A or T
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE: NAME/KEY: allele
LOCATION: 106940 : polymorphic base insertion of A
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE: NAME/KEY: allele
LOCATION: 108106 : polymorphic base insertion of A
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE: NAME/KEY: allele
LOCATION: 108149 : polymorphic base insertion of GTTT
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE: NAME/KEY: allele
LOCATION: 108308 : polymorphic base A or G
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE: NAME/KEY: allele
LOCATION: 108471 : polymorphic base C or T
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE: NAME/KEY: allele
LOCATION: 134134 : polymorphic base C or T
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE: NAME/KEY: allele
LOCATION: 134362 : polymorphic base insertion of A
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE: NAME/KEY: allele
LOCATION: 134374 : polymorphic base insertion of CA
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE: NAME/KEY: allele
LOCATION: 146328 : polymorphic base A or G
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE: NAME/KEY: allele
LOCATION: 146345 : polymorphic base A or C
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE: NAME/KEY: allele
LOCATION: 150329 : polymorphic base A or G
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE: NAME/KEY: allele
LOCATION: 160031 : polymorphic base G or T
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE: NAME/KEY: allele
LOCATION: 72771..72817 : polymorphic fragment 5-124-273 SEQ ID30
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE: NAME/KEY: allele
LOCATION: 80500..80506 : polymorphic fragment 5-127-261 SEQ ID31
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE: NAME/KEY: allele
LOCATION: 88050..88096 : polymorphic fragment 5-127-261 SEQ ID32
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID32
FEATURE: NAME/KEY: allele
LOCATION: 90819..90865 : polymorphic fragment 5-127-261 SEQ ID33
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID33

OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE: NAME/KEY: allele
LOCATION: 90819..90865 : complement polymorphic fragment 99-1437-325 SEQ ID70
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE: NAME/KEY: allele
LOCATION: 93690..93736 : polymorphic fragment 5-128-60 SEQ ID32
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE: NAME/KEY: allele
LOCATION: 93690..93736 : polymorphic fragment 5-128-60 SEQ ID53
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE: NAME/KEY: allele
LOCATION: 97099..97145 : polymorphic fragment 99-1442-224 SEQ ID50
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE: NAME/KEY: allele
LOCATION: 97099..97145 : polymorphic fragment 99-1442-224 SEQ ID71
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE: NAME/KEY: allele
LOCATION: 97130..97177 : polymorphic fragment 5-129-144 SEQ ID33
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE: NAME/KEY: allele
LOCATION: 97130..97177 : polymorphic fragment 5-129-144 SEQ ID54
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE: NAME/KEY: allele
LOCATION: 99075..99121 : polymorphic fragment 5-130-257 SEQ ID34
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE: NAME/KEY: allele
LOCATION: 99075..99121 : polymorphic fragment 5-130-257 SEQ ID55
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE: NAME/KEY: allele
LOCATION: 99094..99140 : polymorphic fragment 5-130-276 SEQ ID35
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE: NAME/KEY: allele
LOCATION: 99094..99140 : polymorphic fragment 5-130-276 SEQ ID56
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE: NAME/KEY: allele
LOCATION: 103783..103828 : polymorphic fragment 5-131-395 SEQ ID36
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE: NAME/KEY: allele
LOCATION: 103783..103828 : polymorphic fragment 5-131-395 SEQ ID57
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE: NAME/KEY: allele
LOCATION: 106918..106966 : polymorphic fragment 5-133-375 SEQ ID37
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE: NAME/KEY: allele
LOCATION: 106918..106966 : polymorphic fragment 5-133-375 SEQ ID58
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE: NAME/KEY: allele
LOCATION: 108084..108130 : polymorphic fragment 5-135-155 SEQ ID38
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE: NAME/KEY: allele
LOCATION: 108084..108130 : polymorphic fragment 5-135-155 SEQ ID59
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE: NAME/KEY: allele
LOCATION: 108127..108177 : polymorphic fragment 5-135-198 SEQ ID39
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39

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FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
NAME/KEY: allele

Query Match          29.5%; Score 35.4; DB 5; Length 162450;
Best Local Similarity 61.3%; Pred. No. 1.7;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 26 agagcggacccctgggagcagaatacttaattcctgactcgtctattatataa 85
Db 82403 atagatgactgtgagccagctgtgtgttgatccctgctcgcactccctg 82462
QY 86 ctaccactcttgccactgtgtgcttaagcttt 118
Db 82463 ctgtgtgactctgtggatggttaactatcttt 82495

RESULT 12
US-09-345-882-1
; Sequence 1, Application US/09345882
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99117
; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
; FEATURE:

NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
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LOCATION: 90819..90865
 OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
 FEATURE:
 NAME/KEY: allele
 LOCATION: 93690..93736
 OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
 FEATURE:
 NAME/KEY: allele
 LOCATION: 93690..93736
 OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
 FEATURE:
 NAME/KEY: allele
 LOCATION: 97099..97145
 OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
 FEATURE:
 NAME/KEY: allele
 LOCATION: 97099..97145
 OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
 FEATURE:
 NAME/KEY: allele
 LOCATION: 97130..97177
 OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
 FEATURE:
 NAME/KEY: allele
 LOCATION: 97130..97177
 OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
 FEATURE:
 NAME/KEY: allele
 LOCATION: 99075..99121
 OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
 FEATURE:
 NAME/KEY: allele
 LOCATION: 99075..99121
 OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
 FEATURE:
 NAME/KEY: allele
 LOCATION: 99094..99140
 OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
 FEATURE:
 NAME/KEY: allele
 LOCATION: 103783..103828
 OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
 FEATURE:
 NAME/KEY: allele
 LOCATION: 103783..103828
 OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
 FEATURE:
 NAME/KEY: allele
 LOCATION: 106918..106966
 OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
 FEATURE:
 NAME/KEY: allele
 LOCATION: 106918..106966
 OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108084..108130
 OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108084..108130
 OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108127..108177
 OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
 FEATURE:
 NAME/KEY: allele
 LOCATION: 108127..108177

OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
 FEATURE:
 NAME/KEY: allele
 Query Match 29.5% Score 35.4; DB 5; Length 162450;
 Best Local Similarity 61.3%; Pred No. 1.7;
 Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 Oy 26 agagcagacctggggaagaatactaaatttaattcctgactgctattttaa 85
 Db 82403 atagatgaactgctggagcagctgctggttggaatccctgctgcaactcctg 82462
 Oy 86 ctaccatcttgccaatgctgctaactttt 118
 Db 82463 ctgtgtgactctggatggttacttaatttt 82495
 RESULT 13
 US-10-126-704-1
 ; Sequence 1, Application US/10126704
 ; GENERAL INFORMATION:
 ; APPLICANT: Bouguetere, Lydie
 ; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-
 ; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
 ; FILE REFERENCE: 44,US,DIY
 ; CURRENT FILING DATE: 2002-04-20
 ; PRIOR APPLICATION NUMBER: US 60/091,315
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/111,909
 ; PRIOR FILING DATE: 1998-12-10
 ; NUMBER OF SEQ ID NOS: 140
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 1
 ; LENGTH: 162450
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 72794
 ; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 88073
 ; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 90842
 ; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 97122
 ; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 99098
 ; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 97152
 ; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 99117
 ; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 103806
 ; OTHER INFORMATION: 5-131-395 : polymorphic base A or T

FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70

NAME/KEY: allele
LOCATION: 93680..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60

```
Query Match          29.5%; Score 35.4; DB 7; Length 162450;
Best Local Similarity 61.3%; Pred. No. 1.7;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 26 agagcagagccttgagcagaataatcgaagtaattcctactctgtattatataa 85
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 82403 atagatgacactgtgagcgaagtgtctgggttgaatccctggtccactcttg 82462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 86 ctaccacattgtccaatgttgcctaagcttt 118
    ||||| ||||| ||||| ||||| |||||
Db 82463 ctgtgtgactctggagatggttacttaattcttt 82495
    ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-027-632-231146
; Sequence 231146, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231146
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-231146

Query Match          29.3%; Score 35.2; DB 7; Length 606;
Best Local Similarity 58.7%; Pred. No. 0.52;
Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

OY 9 gggggtatgcatagaagaagcagacctggagcagaatatcgaagtaattcctg 68
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 500 ggtgtatataatagtgtaagcagcagactctgtgagccaactgcctagtgtaactta 559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 69 acctgctatttaactaactaacattgtgccaatgttgcttaa 112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 gctcattactcttaactctgtgactctgtggccaatgacttaa 603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-984-827-14
; Sequence 14, Application US/09984827
; GENERAL INFORMATION:
; APPLICANT: DENERLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
```

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; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 7379
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-827-14
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```
Query Match          29.3%; Score 35.2; DB 5; Length 7379;
Best Local Similarity 62.5%; Pred. No. 0.94;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 32 ggaacttggagcagaagaataatcgaagtaattcctgaactctgtatttaactaac 91
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1376 gggagtttggagcatacagagctcaagtgaatccctgaacttctactatttgctatat 1435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 92 atcttgcgaatgttgcctaagctttt 119
    ||||| ||||| ||||| ||||| |||||
Db 1436 gaccttgggcaagctgttaagctctct 1463
    ||||| ||||| ||||| ||||| |||||
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Search completed: September 8, 2002, 01:09:44
Job time: 37062 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:31:31 ; Search time 13836.9 Seconds
(without alignments)
187.627 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456
Perfect score: 120
Sequence: 1 taggggaaggggtagtggca.....aatgtgttaagcttttt 120

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

9: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

10: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

11: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

12: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

13: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

14: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

15: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

16: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

17: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

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23: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

24: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

25: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

26: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

27: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

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36: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

37: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

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40: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

41: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

42: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

43: /cgn2_6/ptodata/2/pna/US0806_COMB.seq:*

Result No.	Score	Query	Match Length	ID	Description
1	120	100.0	2877	US-09-834-291-4	Sequence 4, App1
2	120	100.0	3212	US-09-834-291-1	Sequence 1, App1
3	120	100.0	45121	US-09-997-722-10	Sequence 10, App1
4	45.8	38.2	17974	US-60-245-224-9	Sequence 9, App1
5	43.2	36.0	443	US-09-353-690-10171	Sequence 10171, A
6	43.2	36.0	443	US-09-922-340-10171	Sequence 10171, A
7	43.2	36.0	443	US-09-922-340A-10171	Sequence 10171, A
8	43.2	36.0	518	US-09-726-803-609	Sequence 609, App
9	43.2	36.0	684	US-09-726-803-1202	Sequence 1202, App
10	42.8	35.7	11532	US-60-205-418-135	Sequence 135, App
11	42.8	35.7	396	US-09-824-559-1994	Sequence 1994, App
12	41.6	34.7	32768	US-60-207-583-151	Sequence 151, App
13	41.6	34.7	32768	US-60-230-445-984	Sequence 984, App
14	41.6	34.7	143899	US-09-972-546-15	Sequence 15, App1
15	40.6	33.8	4041	US-60-212-358-85	Sequence 85, App1
16	40.6	33.8	136163	US-60-226-176-1053	Sequence 1053, App
17	40.6	33.8	136163	US-60-233-468-1053	Sequence 1053, App
18	40.6	33.8	136163	US-60-313-371-1053	Sequence 1053, App
19	40.6	33.8	151471	US-60-226-176-239	Sequence 239, App
20	40.6	33.8	151471	US-60-233-468-239	Sequence 239, App
21	40.6	33.8	151471	US-60-313-371-239	Sequence 239, App
22	40.4	33.7	79312	US-60-242-679-393	Sequence 393, App
23	39	32.5	262	PCR-US01-15674A-99	Sequence 99, App1
24	39	32.5	262	US-09-234-119A-145	Sequence 145, App
25	39	32.5	262	US-09-573-080A-99	Sequence 99, App1
26	39	32.5	359	US-09-428-151A-2422	Sequence 2422, App
27	39	32.5	359	US-09-614-387-1897	Sequence 1897, App
28	39	32.5	13964	US-60-230-445-917	Sequence 917, App
29	39	32.5	23659	US-60-206-020-98	Sequence 98, App1
30	39	32.5	216504	US-60-242-679-316	Sequence 316, App
31	38.8	32.3	32768	US-60-213-177-302	Sequence 302, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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32 38.8 32.3 32768 62 US-60-230-445-490 Sequence 490, App
33 38.8 32.3 32768 62 US-60-233-937-211 Sequence 211, App
34 38.4 32.0 9613 1 PCT-US01-01334-8121 Sequence 8121, App
35 38.4 32.0 9613 30 US-09-764-874-8121 Sequence 8121, App
36 38.4 32.0 9613 37 US-10-092-400-8121 Sequence 8121, App
37 38.4 32.0 9614 1 PCT-US01-01334-8123 Sequence 8123, App
38 38.4 32.0 9614 30 US-09-764-874-8123 Sequence 8123, App
39 38.4 32.0 9614 37 US-10-092-400-8123 Sequence 8123, App
40 38.4 32.0 112392 63 US-60-245-228-209 Sequence 209, App
41 38.4 32.0 112392 64 US-60-258-272-83 Sequence 83, App
42 38.2 31.8 576 24 US-09-637-889-5424 Sequence 5424, App
43 38 31.7 633 24 US-09-634-306B-281585 Sequence 281585, App
44 38 31.7 32768 59 US-60-208-084-23 Sequence 23, App
45 38 31.7 32768 59 US-60-208-596-27 Sequence 27, App
```

ALIGNMENTS

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RESULT 1
US-09-834-291-4
; Sequence 4, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4
```

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Query Match 100.0%; Score 120; DB 32; Length 2827;
Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 taggggaagggtatgcatagaaagcagaccttgggaagaagaatacttaagttt 60
Db 337 taggggaagggtatgcatagaaagcagaccttgggaagaagaatacttaagttt 396
QY 61 aattcctgactctgctatttataactaacacatcttggccaatgttgccttaagctttt 120
Db 397 aattcctgactctgctatttataactaacacatcttggccaatgttgccttaagctttt 456
```

```
RESULT 2
US-09-834-291-1
; Sequence 1, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
```

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; SEQ ID NO 1
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1
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Query Match 100.0%; Score 120; DB 32; Length 3212;
Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 taggggaagggtatgcatagaaagcagaccttgggaagaagaatacttaagttt 60
Db 337 taggggaagggtatgcatagaaagcagaccttgggaagaagaatacttaagttt 396
QY 61 aattcctgactctgctatttataactaacacatcttggccaatgttgccttaagctttt 120
Db 397 aattcctgactctgctatttataactaacacatcttggccaatgttgccttaagctttt 456
```

```
RESULT 3
US-09-997-722-10
; Sequence 10, Application US/09997722
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCP
; CURRENT APPLICATION NUMBER: US/09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 10
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-10
```

```
Query Match 100.0%; Score 120; DB 36; Length 45121;
Best Local Similarity 100.0%; Pred. No. 4.3e-26;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 taggggaagggtatgcatagaaagcagaccttgggaagaagaatacttaagttt 60
Db 8330 taggggaagggtatgcatagaaagcagaccttgggaagaagaatacttaagttt 8389
QY 61 aattcctgactctgctatttataactaacacatcttggccaatgttgccttaagctttt 120
Db 8390 aattcctgactctgctatttataactaacacatcttggccaatgttgccttaagctttt 8449
```

```
RESULT 4
US-60-245-224-9/C
; Sequence 9, Application US/60245224
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: C1000887
; CURRENT APPLICATION NUMBER: US/60/245,224
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 17974
; TYPE: DNA
; ORGANISM: HUMAN
```


US-60-245-224-9

Query Match 38.2%; Score 45.8; DB 63; Length 17974;
Best Local Similarity 64.8%; Pred. No. 0.0034;
Matches 68; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 15 atggcctagaagagagacgttggaagaataatcattatcctgactg 74

DB 14562 ATCTGTAGTAACACATTAATCTGGCGCAGACACTAAGCTCAATCTGATTG 14503

QY 75 ctatttaactaacacattcttgccaatgttgcttaagctttt 119

DB 14502 CTAATTCTCAAGCTGTGTAACCTGGAATAATGCTTAACCTCTCT 14458

RESULT 5

US-09-353-690-10171/c

Sequence 10171, Application US/09353690

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

FILE REFERENCE: 20411-726CON2

CURRENT APPLICATION NUMBER: US/09/353,690

EARLIER FILING DATE: 1999-07-14

EARLIER APPLICATION NUMBER: US 09/217,517

EARLIER FILING DATE: 1998-12-22

EARLIER APPLICATION NUMBER: US 09/004,182

NUMBER OF SEQ ID NOS: 12181

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10171

LENGTH: 443

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)...(443)

OTHER INFORMATION: n = A,T,C or G

US-09-353-690-10171

Query Match 36.0%; Score 43.2; DB 17; Length 443;

Best Local Similarity 60.0%; Pred. No. 0.0071;

Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 taggggaagggtatgcatagaagaagagacgttggaagaataatcatt 60

DB 146 TGGAGGAAATGAAAGCAATATCGAGAGCCTGGGCTGTGCATCAGATGCTGAGTTC 87

QY 61 aatccgactctgctatttataactaacacattcttgccaatgttgcttaagctttt 120

DB 86 AAACCTGCTCTGCTTTTGTGTAACCTGTGACCTTTGGGCAAGTCCCTTAACCTCTCTT 27

RESULT 6

US-09-922-340-10171/c

Sequence 10171, Application US/09922340

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

FILE REFERENCE: 20411-726CON2

CURRENT APPLICATION NUMBER: US/09/922,340

EARLIER FILING DATE: 2001-08-03

EARLIER APPLICATION NUMBER: US/09/353,690

EARLIER FILING DATE: 1999-07-14

EARLIER APPLICATION NUMBER: US 09/004,182

NUMBER OF SEQ ID NOS: 12181

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10171

LENGTH: 443

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)...(443)

OTHER INFORMATION: n = A,T,C or G

US-09-922-340-10171

Query Match 36.0%; Score 43.2; DB 34; Length 443;

Best Local Similarity 60.0%; Pred. No. 0.0071;

Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 taggggaagggtatgcatagaagaagagacgttggaagaataatcatt 60

DB 146 TGGAGGAAATGAAAGCAATATCGAGAGCCTGGGCTGTGCATCAGATGCTGAGTTC 87

QY 61 aatccgactctgctatttataactaacacattcttgccaatgttgcttaagctttt 120

DB 86 AAACCTGCTCTGCTTTTGTGTAACCTGTGACCTTTGGGCAAGTCCCTTAACCTCTCTT 27

RESULT 7

US-09-922-340A-10171/c

Sequence 10171, Application US/09922340A

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained

FILE REFERENCE: 20411-726CON2

CURRENT APPLICATION NUMBER: US/09/922,340A

EARLIER FILING DATE: 2001-08-03

EARLIER APPLICATION NUMBER: US/09/353,690

EARLIER FILING DATE: 1999-07-14

EARLIER APPLICATION NUMBER: US 09/217,517

EARLIER FILING DATE: 1998-12-22

EARLIER APPLICATION NUMBER: US 09/004,182

NUMBER OF SEQ ID NOS: 12181

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10171

LENGTH: 443

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)...(443)

OTHER INFORMATION: n = A,T,C or G

US-09-922-340A-10171

Query Match 36.0%; Score 43.2; DB 34; Length 443;

Best Local Similarity 60.0%; Pred. No. 0.0071;

Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 taggggaagggtatgcatagaagaagagacgttggaagaataatcatt 60

DB 146 TGGAGGAAATGAAAGCAATATCGAGAGCCTGGGCTGTGCATCAGATGCTGAGTTC 87

QY 61 aatccgactctgctatttataactaacacattcttgccaatgttgcttaagctttt 120

DB 86 AAACCTGCTCTGCTTTTGTGTAACCTGTGACCTTTGGGCAAGTCCCTTAACCTCTCTT 27

RESULT 8

US-09-726-803-609

Sequence 609, Application US/09726803

GENERAL INFORMATION:

APPLICANT: Geating, David P.

APPLICANT: Holtzman, Douglas A.

APPLICANT: Kingsbury, Gillian A.

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

```
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: 1600.2050-001
;; CURRENT APPLICATION NUMBER: US/09/726,803
;; CURRENT FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: 60/168,085
;; PRIOR FILING DATE: 1999-11-30
;; NUMBER OF SEQ ID NOS: 1769
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 609
;; LENGTH: 518
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(518)
;; OTHER INFORMATION: n = A,T,C or G
US-09-726-803-609
```

```
Query Match          36.0%; Score 43.2; DB 29; Length 518;
Best Local Similarity 65.6%; Pred. No. 0.0075;
Matches 63; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
```

```
QY 24 aaagacgagccttgggagcaagaatacttaattcctgactctgtattatt 83
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 389 aagagacgtgacttgcagctacagctgctagttagaactcctgctctgcatgtatt 448
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 aactaacatcttgcacatgttgccttaagctttt 119
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 449 agtcatgtgccttgcctgtcatgttacttaacctttct 484
```

```
RESULT 9
US-09-726-803-1202
; Sequence 1202, Application US/09726803
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2050-001
; CURRENT APPLICATION NUMBER: US/09/726,803
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,085
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 1769
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1202
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-803-1202
```

```
Query Match          36.0%; Score 43.2; DB 29; Length 684;
Best Local Similarity 65.6%; Pred. No. 0.0081;
Matches 63; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
```

```
QY 24 aaagacgagccttgggagcaagaatacttaattcctgactctgtattatt 83
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 aagagacgtgacttgcagctacagctgacttagttagaactcctgctctgcatgtatt 585
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 84 aactaacatcttgcacatgttgccttaagctttt 119
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 586 agtcatgtgccttgcctgtcatgttacttaacctttct 621
```

```
RESULT 10
US-60-205-418-135
; Sequence 135, Application US/60205418
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
```

```
;; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
;; FILE REFERENCE: NOVEL NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
;; TITLE OF INVENTION: US/09/726,803
;; FILE REFERENCE: CL000556
;; CURRENT APPLICATION NUMBER: US/60/205,418
;; CURRENT FILING DATE: 2000-05-19
;; NUMBER OF SEQ ID NOS: 536
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 135
;; LENGTH: 11532
;; TYPE: DNA
;; ORGANISM: HUMAN
US-60-205-418-135
```

```
Query Match          36.0%; Score 43.2; DB 59; Length 11532;
Best Local Similarity 60.0%; Pred. No. 0.019;
Matches 72; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
```

```
QY 1 taggggaagggggtagatgcataagaagcagacccctgggagcaagaatacttaagtt 60
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6451 tggaggaatgaaaggaatactgcagagcctggtgctctgcataagaatgcctgattc 6510
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 aatcctgactctgtatttacttaactaacatcttgcacatgttgccttaagcttttt 120
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6511 aaacctgtctctgtcttcttgccttaactgtgacttggcaggaagtcacttaacctctt 6570
```

```
RESULT 11
US-09-824-559-1994
; Sequence 1994, Application US/09824559
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Jakubowski, Joseph A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2077-001
; CURRENT APPLICATION NUMBER: US/09/824,559
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,437
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9929
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1994
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-824-559-1994
```

```
Query Match          35.7%; Score 42.8; DB 31; Length 396;
Best Local Similarity 66.0%; Pred. No. 0.0092;
Matches 62; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
QY 25 aagagacgagccttgggagcaagaatacttaattcctgactctgtattatt 84
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 151 aagagcgtgaagttgggaacacagacgtctggaatttaacttaaccttaacctattat 210
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 aactaacatcttgcacatgttgccttaagctttt 118
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 211 gctgtgtgactttaggaagttacttaacctttct 244
```

```
RESULT 12
US-60-207-583-151/C
; Sequence 151, Application US/60207583
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CL000598
```

RESULT 15
US-60-212-358-85
; Sequence 85, Application US/60212358

```

: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
: TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
: TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
: FILE REFERENCE: CLO00684
: CURRENT APPLICATION NUMBER: US/60/212,358
: CURRENT FILING DATE: 2000-06-19
: NUMBER OF SEQ ID NOS: 324
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 85
: LENGTH: 4041
: TYPE: DNA
: ORGANISM: HUMAN
: US-60-212-358-85

```

QY	25	aagagcagactctgggggcaagaatctactaagttaattcttcgtactgcgcatttata	84
Db	2183	aagagcagatggccctcgaaagacagatcacttaagctcaaatccgtatctcgctcaattca	2242
QY	85	actaacctctcttgccaagtgttgcttaagctttt	119
Db	2243	actgtgtaacctcgagacacttacttaactctctc	2277

Search completed: September 7, 2002, 22:31:46
Job time: 43800 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:07 ; Search time 212.3 Seconds
(without alignments)
138.841 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456

Perfect score: 120

Sequence: 1 taagggaagggggtatggca.....aatgttctaagcttttt 120

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Packfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	32.2	26.8	10564	1 US-08-206-176-5	Sequence 5, Appli
C 2	30.6	25.5	1980	2 US-08-766-858A-4	Sequence 4, Appli
C 3	28.6	23.8	2369	1 US-07-797-556-1	Sequence 1, Appli
C 4	28.6	23.8	2369	1 US-08-308-881-1	Sequence 1, Appli
C 5	28.6	23.8	2369	2 US-09-058-263-1	Sequence 1, Appli
C 6	28.6	23.8	2369	2 US-09-059-099-1	Sequence 1, Appli
C 7	28.6	23.8	2369	3 US-09-058-264-1	Sequence 1, Appli
C 8	28.6	23.8	2369	5 PCT-US95-06530-1	Sequence 1, Appli
C 9	28.6	23.8	3085	4 US-08-795-473B-4	Sequence 4, Appli
C 10	28.2	23.5	87350	3 US-08-781-891-79	Sequence 79, Appli
C 11	28	23.3	2517	3 US-08-733-360A-4	Sequence 4, Appli
C 12	28	23.3	2517	3 US-08-987-743-16	Sequence 16, Appli
C 13	28	23.3	2517	4 US-08-916-935-4	Sequence 4, Appli
C 14	28	23.3	5873	1 US-07-928-464-4	Sequence 4, Appli
C 15	28	23.3	5873	5 PCT-US93-07347-4	Sequence 4, Appli
C 16	28	23.3	5890	1 US-07-928-464-3	Sequence 3, Appli
C 17	28	23.3	5890	1 US-07-928-464-5	Sequence 5, Appli
C 18	28	23.3	5890	1 US-07-928-464-6	Sequence 6, Appli
C 19	28	23.3	5890	5 PCT-US93-07347-3	Sequence 3, Appli
C 20	28	23.3	5890	5 PCT-US93-07347-5	Sequence 5, Appli
C 21	28	23.3	5890	5 PCT-US93-07347-6	Sequence 6, Appli
C 22	28	23.3	6295	1 US-08-003-311B-4	Sequence 4, Appli
C 23	28	23.3	6295	1 US-08-261-432-4	Sequence 4, Appli
C 24	28	23.3	6312	1 US-08-003-311B-3	Sequence 3, Appli
C 25	28	23.3	6312	1 US-08-003-311B-5	Sequence 5, Appli
C 26	28	23.3	6312	1 US-08-003-311B-6	Sequence 6, Appli
C 27	28	23.3	6312	1 US-08-003-311B-7	Sequence 7, Appli

C 28	28	23.3	6312	1 US-08-261-432-3	Sequence 3, Appli
C 29	28	23.3	6312	1 US-08-261-432-5	Sequence 5, Appli
C 30	28	23.3	6312	1 US-08-261-432-6	Sequence 6, Appli
C 31	28	23.3	6312	1 US-08-261-432-7	Sequence 7, Appli
C 32	27.8	23.2	1679	1 US-08-202-056-6	Sequence 6, Appli
C 33	27.8	23.2	1679	1 US-08-076-093A-5	Sequence 5, Appli
C 34	27.8	23.2	1679	1 US-08-701-265-5	Sequence 5, Appli
C 35	27.8	23.2	1679	2 US-08-284-586-5	Sequence 5, Appli
C 36	27.8	23.2	1679	2 US-08-805-478-5	Sequence 5, Appli
C 37	27.8	23.2	1679	2 US-08-802-627A-5	Sequence 5, Appli
C 38	27.8	23.2	1679	2 US-08-801-238-5	Sequence 5, Appli
C 39	27.8	23.2	1679	2 US-08-801-238-5	Sequence 5, Appli
C 40	27.8	23.2	1679	3 US-09-104-296-5	Sequence 5, Appli
C 41	27.8	23.2	1679	5 PCT-US94-06380-3	Sequence 3, Appli
C 42	27.6	23.0	59065	4 US-09-813-817-3	Sequence 3, Appli
C 43	27.2	22.7	867	4 US-09-273-839A-7	Sequence 7, Appli
C 44	27.2	22.7	2160	1 US-08-082-849B-30	Sequence 30, Appli
C 45	27.2	22.7	2160	5 PCT-US94-01624-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1
US-08-206-176-5/C
Sequence 5, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Dairymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: human fibrinogen gamma chain
FEATURE:
NAME/KEY: CDS
LOCATION: join(1799..1876, 1973..2017, 2207..2390, 2510
..2603, 4211..4541, 4645..4778, 5758..5942, 7426
LOCATION: ..7703, 9342..9571)
US-08-206-176-5


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RESULT      5
US-09-058-263-1
; Sequence 1, Application US/09058263
; Patent No. 5891997
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,263
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TEXT: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; TISSUE TYPE: human placenta
; IMMEDIATE SOURCE:
; CLONE: B106/PDC303
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2369
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 310..2369
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 244..309
; US-09-058-263-1

Query Match      23.8%; Score 28.6; DB 2; Length 2369;
Best Local Similarity 55.6%; Pred. No. 1.2;
Matches 55; Conservative 0; Mismatches 44; Indels 0; Gaps 0

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Db      150 atggaagaaagcagacatttagaagtagaagacttagcttgaattcccttactctt 209

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QY 80 tattaactaaccaatctttgccaatgttgcttaagcttt 118
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RESULT 6
HS-09-059-

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US-09-059-099-1
Sequence 11, Application US/09059099
Patent No. 5925740
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,099
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-09-059-099-1

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Query Match	23.8%	Score 28.6;	DB 2;	Length 2369;
Best Local Similarity	55.6%;	Pred. No. 1.2;		
Matches	55;	Conservative	0;	Mismatches 44;
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RESULT 7

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US-09-058-264-1
? Sequence 1, Application US/09058264
? Patent No. 6010886
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? GENERAL INFORMATION:
?
? APPLICANT: Mosley, Bruce
?
? APPLICANT: Cosman, David J.
?
? TITLE OF INVENTION: Receptor for Oncostatin M
?
? NUMBER OF SEQUENCES: 11
?
? CORRESPONDENCE ADDRESS:
?
? ADDRESSEE: Immunex Corporation
?
? STREET: 51 University Street
?
? City: Seattle
?
? STATE: WA
?
? COUNTRY: USA
?
? ZIP: 98101
?
? COMPUTER READABLE FORM:
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? MEDIUM TYPE: Floppy disk
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? COMPUTER: Apple Macintosh
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? OPERATING SYSTEM: Apple 7.1
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? SOFTWARE: Microsoft Word, Version 5.1a
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? CURRENT APPLICATION DATA:
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? APPLICATION NUMBER: US/09/058,264
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? FILING DATE:
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? CLASSIFICATION:
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? PRIOR APPLICATION DATA:
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? APPLICATION NUMBER: US/08/308,881
?
? FILING DATE: 12-SEP-1994
?
? APPLICATION NUMBER: US 08/249,553
?
? FILING DATE: 26-MAY-1994
?
? ATTORNEY/AGENT INFORMATION:
?
? NAME: Seese, Kathryn A.
?
? REGISTRATION NUMBER: 32,172
?
? REFERENCE/DOCKET NUMBER: 2614-A
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: (206) 587-0430
?
? TELEFAX: (206) 233-0644
?
? TELEX: 756882
?
? INFORMATION FOR SRO ID NO: 1:
?
? SEQUENCE CHARACTERISTICS:
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? LENGTH: 2369 base pairs
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? TYPE: nucleic acid
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? STRANDEDNESS: single
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? TOPOLOGY: linear
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? MOLECULE TYPE: cDNA to mRNA
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? HYPOTHETICAL: NO
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? ANTI-SENSE: NO
?
? FRAGMENT TYPE: N-terminal
?
? ORIGINAL SOURCE:
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? TISSUE TYPE: human placenta
?
? IMMEDIATE SOURCE:
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? CLONE: B10G/PDC303
?
? FEATURE:
?
? NAME/KEY: CDS
?
? LOCATION: 244..2369
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? FEATURE:
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? NAME/KEY: mat.peptide
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? LOCATION: 310..2369
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? FEATURE:
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? NAME/KEY: sig.peptide
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? LOCATION: 244..309
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? US-09-058-264-1

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; NAME/KEY: sig_peptide
; LOCATION: 244..309
US-09-058-264-1

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RESULT 10
US-08-781-891-79/c
Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-79

Query Match 23.5%; Score 28.2; DB 3; Length 87350;
Best Local Similarity 54.3%; Pred. No. 5.5;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 3 ggggaaggggtatgcatagaagagcagaccttgggaagaatataatcttaagttaa 62
DB 76618 gttgaagccatnccacagatggcatgctatagagatccctcagctgggttga 76559
QY 63 ttcttacttgcattattataaaccatttgcacatgttg 107
DB 76558 atcctgctctgccgcttactaataatagcaatctaggaattatng 76514

RESULT 11
US-08-733-360A-4/c
Sequence 4, Application US/08733360A
Patent No. 6103525
GENERAL INFORMATION:
APPLICANT: Stern, Robert
APPLICANT: Frost, Gregory
APPLICANT: Csoka, Anthony
APPLICANT: Wong, Tim M.
TITLE OF INVENTION: Human Plasma Hyaluronidase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol L. Francis, Ph.D.
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,360A
FILING DATE: 17-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L.
REGISTRATION NUMBER: 36,513
REFERENCE/DOCKET NUMBER: 06510/063001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 327-3400
TELEFAX: (650) 327-3231
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-733-360A-4

Query Match 23.3%; Score 28; DB 3; Length 2517;
Best Local Similarity 55.0%; Pred. No. 2;
Matches 55; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 16 tggcatagaagagcagaccttgggaagaatataatcttaagttaattcctgactctgc 75
DB 2432 tagagatgcaaggcctgtaccccgagctagacagcctgggttgatctgaactctgc 2373
QY 76 tattattaaactaacatcttgcacatgttgcttaagt 115
DB 2372 cctttcttctgtgcaaccttgaggcaactgtcttactct 2333

RESULT 12
US-08-987-743-16/c
Sequence 16, Application US/08987743
Patent No. 6123938
GENERAL INFORMATION:
APPLICANT: Stern, Robert
APPLICANT: Csoka, Anthony
APPLICANT: Frost, Gregory I.
APPLICANT: Wong, Tim M.
TITLE OF INVENTION: Purification and Microsequencing of
FILE REFERENCE: 9076/088CIP2
CURRENT APPLICATION NUMBER: US/08/987,743
EARLIER FILING DATE: 1997-12-09
EARLIER APPLICATION NUMBER: 08/733,360
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 2517
TYPE: DNA
ORGANISM: H. sapiens
US-08-987-743-16

Query Match 23.3%; Score 28; DB 3; Length 2517;
Best Local Similarity 55.0%; Pred. No. 2;
Matches 55; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 16 tggcatagaagagcagaccttgggaagaatataatcttaagttaattcctgactctgc 75

Db 2432 TAGAGTGAAGGCTGTACCCCGAGCTAGACAGCTGGGTTTGAATCTCACTTCTC 2373
QY 76 tattattactaaccacatttgcgaatgttgcctaagct 115
2372 CCTTTCTTGCTGTGCAACCTTGGGCAACGTCCTACTCT 2333

RESULT 13
US-08-916-935-4/c
; Sequence 4, Application US/08916935
; Patent No. 6193963
; GENERAL INFORMATION:
; APPLICANT: Stern, Robert
; APPLICANT: Prost, Gregory I.
; APPLICANT: Csoka, Anthony
; APPLICANT: Wong, Tim. M.
; TITLE OF INVENTION: Human Plasma Hyaluronidase
; FILE REFERENCE: 9076-088CIP
; CURRENT APPLICATION NUMBER: US/08/916,935
; EARLIER FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-916-935-4

Query Match 23.3%; Score 28; DB 4; Length 2517;
Best Local Similarity 55.0%; Pred. No. 2;
Matches 55; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 16 tggcagaagaagcaggaccttggagcaagaatacttaattcctgactcgc 75
Db 2432 TAGAGTGAAGGCTGTACCCCGAGCTAGACAGCTGGGTTTGAATCTCACTTCTC 2373

QY 76 tattattactaaccacatttgcgaatgttgcctaagct 115
Db 2372 CCTTTCTTGCTGTGCAACCTTGGGCAACGTCCTACTCT 2333

RESULT 14
US-07-928-464-4/c
; Sequence 4, Application US/07928464
; Patent No. 5367065
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/928,464
; FILING DATE: 19920810
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.

REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5873 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-928-464-4

Query Match 23.3%; Score 28; DB 1; Length 5873;
Best Local Similarity 60.5%; Pred. No. 2.6;
Matches 46; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 8 agggggtatgcatagaagagcagcacttggagcaagaatatcctaattcct 67
Db 4181 AAGAGGAATAAATATCAAAATCAAAACATTTGACACACAAATTTCTAATTGATTCAA 4122

QY 68 gactcgcctattatt 83
Db 4121 ACCTTGACTGTATTATT 4106

RESULT 15
PCT-US93-07347-4/c
; Sequence 4, Application PC/TUS9307347
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R.
; APPLICANT: Kieber, Joseph J.
; TITLE OF INVENTION: Constitutive Triple Response Gene and
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07347
; FILING DATE: 19930805
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Suzanne E.
; REGISTRATION NUMBER: 32,279
; REFERENCE/DOCKET NUMBER: UPN-1086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-07347-4

Query Match 23.3%; Score 28; DB 5; Length 5873;
Best Local Similarity 60.5%; Pred. No. 2.6;
Matches 46; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
180.856 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38.4	32.0	9613	22	ABA15790	Human nervous syst
2	38.4	32.0	9614	22	ABA15792	Human nervous syst
3	36	30.0	59060	22	AAK85994	Human Immune/haema
4	35.8	29.8	13046	22	AAI03250	Human Reproductive
5	35.8	29.8	13046	22	AAH31516	Human DNA for a no
6	35.8	29.8	160755	23	AAH88704	Human DNA sequence
7	35.4	29.5	162450	21	AAH8967	Retinoblastoma bin
8	35.2	29.3	7052	21	AAH69140	Human ABC1 gene ex
9	35.2	29.3	9519	22	AAU37169	Human musculoskele

C	10	35.2	29.3	14537	22	AAH46356	Tumour suppressor
C	11	35.2	29.3	56632	22	AAK65581	Human Immune/haema
C	12	35.2	29.3	183999	22	AAH92831	Human ABC1 genomic
C	13	34.8	29.0	267	22	AAI13265	Human breast cancer
C	14	34.2	28.5	305	22	AAI22135	Human breast cancer
C	15	34.2	28.5	4171	22	AAI36300	Human musculoskele
C	16	34.2	28.5	13819	22	ABA15398	Human nervous syst
C	17	34.2	28.5	15944	22	ABA15399	Human nervous syst
C	18	34	28.3	615	22	AAK57137	Human Immune/haema
C	19	34	28.3	22473	22	AAK71400	Human Immune/haema
C	20	33.8	28.2	3952	22	AAH30046	Human lung antigen
C	21	33.4	27.8	5424	21	AAH21243	Human low adenostin
C	22	33.4	27.8	5424	21	AAH35121	Human adenostin re
C	23	33.4	27.8	5845	24	AAH33663	Human Immune syste
C	24	33.4	27.8	17425	20	AAH28366	Human Stat6 gene.
C	25	33.4	27.8	19301	21	AAH21245	Human low adenostin
C	26	33.4	27.8	19301	21	AAH35123	Human adenostin re
C	27	33.4	27.8	23071	22	AAH26699	Human genomic DNA
C	28	33.2	27.7	11130	22	ABA15386	Human nervous syst
C	29	33	27.5	39796	21	AAH61681	Nucleotide sequenc
C	30	32.6	27.2	613	22	AAH82020	Human Immune/haema
C	31	32.6	27.2	1427	22	AAH19199	Human secreted pro
C	32	32.6	27.2	1964	22	AAH94698	Human full-length
C	33	32.6	27.2	2496	22	AAH19170	Human secreted pro
C	34	32.6	27.2	10085	22	AAH42054	Genomic sequence #
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C	36	32.4	27.0	200	18	AAH89469	CFTR gene regulato
C	37	32.4	27.0	575	22	ABA61508	Human foetal liver
C	38	32.4	27.0	575	22	AAH29230	Probe #7696 for ge
C	39	32.4	27.0	575	22	AAH09808	Human brain expres
C	40	32.4	27.0	575	22	AAH35702	Human bone marrow
C	41	32.4	27.0	575	22	AAH17107	Probe #7040 for ge
C	42	32.4	27.0	575	22	AAH14117	Probe #10103 used
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C	44	32.2	26.8	1497	22	AAH27793	Human TANGO 295 co
C	45	32.2	26.8	2035	24	ABA02080	Human YSKI protein

ALIGNMENTS

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DT	23-JAN-2002	(first entry)
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KW	antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;	
KW	antirheumatic; hepatotropic; cerebropotective; antinflammatory;	
KW	antiallergic; antidiabetic; antilucifer; anticonvulsant; antitungal;	
KW	antiparasitic; cardiant; immune disorder; cardiovascular disorder;	
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.	
OS	Homo sapiens.	
XX		
PN	WO200159063-A2.	
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 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM:
 WPI: 2001-541565/60.
 Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 useful for preventing, diagnosing and/or treating nervous system
 cancers and metastases -
 Disclosure: SEQ ID NO 8121; 1701pp + Sequence Listing; English.
 The invention relates to novel genes (ABA11004-ABA21534) and proteins
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 medical conditions e.g. by protein or gene therapy. The genes are

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PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

XX PA
XX PI Rosen CA, Barash SC, Ruben SM;
XX DR WPI; 2001-541565/60.

XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
PS
XX

Disclosure: SEQ ID NO 8123; 1701pp + Sequence Listing; English.

XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABAI678-ABAI8001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification..
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischemias;

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AC AAL03250;
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DT 21-NOV-2001 (first entry)
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KW Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
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OS Homo sapiens.
XX
PN MO200155320-A2.
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PR 29-SEP-2000; 2000US-0236369.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
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PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249244.


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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
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PR 20-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244826.
PR 08-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249219.
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PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
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PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251989.
PR 05-DEC-2000; 2000US-0251990.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX

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PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465572/50.
XX
PT Nucleic acid molecules encoding human secreted extracellular matrix
PT proteins, used in preventing, treating or ameliorating a disorder, e.g.
PT Alzheimer's and Parkinson's diseases and cancers -
XX
PS
XX
XX Claim 1; SEQ ID NO 595; 577bp; English.
XX
XX The invention relates to isolated nucleic acid molecules encoding
XX novel human secreted extracellular matrix proteins (SPs). The
XX polynucleotides and proteins are used to prevent, treat a medical
XX condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
XX chickens or sheep. For example, disorders associated with decreased
XX expression of SPs. The SP polynucleotide or a vector expressing them may
XX be administered to treat diseases by gene therapy. Antisense molecules
XX may be administered to down regulate expression of SPs by binding with
XX the cells own genes and preventing their expression. The polynucleotides
XX may also be used as DNA probes in diagnostic assays. The SPs may also be
XX used as antigens to produce antibodies and to identify modulators
XX (agonists and antagonists) of the SPs. The anti-(SP) antibodies and
XX antagonists may also be used to down regulate expression and activity of
XX SP and as diagnostic agents for detecting the presence of SPs in samples.
XX
XX The disorders include for example: immune/autoimmune diseases (e.g. HIV
XX (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
XX and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
XX melanomas, neoplasms of the breast or liver, Sezary syndrome and
XX Parkinson's disease), cardiovascular diseases (e.g. Alzheimer's disease,
XX arrest, tachycardia and angina), infections caused by bacteria, viruses
XX and fungi and ocular disorders (e.g. corneal infections). Other uses
XX include wound healing, maintenance of organs before transplantation,
XX support of cell culture of primary tissues, modulation of for example
XX
XX
XX Query Match 29.8%; Score 35.8; DB 22; Length 13046;
XX Best Local Similarity 61.1%; Pred. No. 0.12;
XX Matches 58; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
XX
XX QY 25 aagagcaggaccttggagcaagataatcctaattcctgcgtactatattatla 84
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 8107 AAAAGCAGCGACTGCTGCAACCACTGCTGATTTGATCTACTCTGCCAATTAC 8048
XX
XX QY 85 actaacatcttgcacatgttgccttaagctttt 119
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 8047 ACTGTGTGACCTTGCGCAAGTTACTTACTTCTCT 8013
XX
XX RESULT 6
XX AAH88704/C
XX ID AAH88704 standard; DNA; 160755 BP.
XX
XX AAH88704;
XX
XX AC 26-FEB-2002 (first entry)
XX
XX DT
XX XX
XX DE Human DNA sequence SEQ ID 544.
XX
XX KW Single nucleotide polymorphism; SNP; diallelic marker; human;
XX central nervous system disorder; CNS; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200151659-A2.
XX
XX XX
XX PD 19-JUL-2001.
XX
XX PF 11-JAN-2001; 2001MO-IB00116.
XX
XX PR 13-JAN-2000; 2000US-0175854.
XX
XX

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PA (GEST) GENSET.
XX Chu T, Blumenfeld M, Cohen D;
XX WPI: 2001-483085/52.
DR
XX Isolated polynucleotides, useful for genotyping nucleic acids for
PT biallelic markers for the diagnosis of depression, comprises central
PT nervous system disorder related biallelic marker
XX
PS Disclosure: Page 476-519; 519pp; English.
XX
XX The present invention relates to biallelic markers derived from human
CC genes involved in central nervous system (CNS) disorders (see
CC AAH8161-AAH8702). The markers have a single nucleotide polymorphism
CC (SNP) and are useful in determining the genetic predisposition of
CC individuals to CNS disorders, by identifying the nucleotides at a set of
CC genetic markers in a biological sample, where the markers comprise at
CC least one CNS disorder related marker. The present sequence was used
CC to illustrate the invention.
XX
SO Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other:
XX
Query Match 29.8%; Score 35.8; DB 23; Length 160755;
Best Local Similarity 57.7%; Pred. No. 0.27;
Matches 64; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
OY 9 ggggtaagcctagaagaagcagaccttgagagcaagataatctaagttattctctg 68
DB 144773 GTGGATGTTGCTAAGATGAGCATGTGGAACCAAGATTAACGTCATCTGAAGCCTG 144714
OY 69 atccgcattattactaacaccatcttgccaatgttgcttaagctttt 119
DB 144713 GCTCGCTACTACTACTGCTGGAGATTTCACCTGTGGGCTCAGTTTCT 144663
RESULT 7
AAZ86967
ID AAZ86967 standard; DNA; 162450 BP.
XX
XX AAZ86967;
XX
XX 16-MAY-2000 (first entry)
DE Retinoblastoma binding protein-7 genomic DNA sequence.
XX
XX RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
KW diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
KW benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
XX lymphoma; ds.
XX
XX Homo sapiens.
OS
XX WO200000607-A1.
XX
XX 06-JAN-2000.
PD
XX 30-JUN-1999; 99WO-1B01242.
PF
XX 30-JUN-1998; 98US-0091315.
PR 10-DEC-1998; 98US-0111909.
XX
XX (GEST) GENSET.
PA
XX Bougueleret L;
PI
XX WPI: 2000-117170/10.
DR
XX Novel nucleic acid and polymorphic markers used for diagnosis of
PT diseases, especially those involving abnormal cell proliferation and
PT differentiation -
XX

PS Claim 1; Page 118-163; 223pp; English.
XX
XX This sequence represents the retinoblastoma binding protein-7 (RBP-7)
CC genomic sequence of the invention. The RBP-7 coding sequence and
CC regulatory sequences are useful for the recombinant production of the
CC protein and for expressing heterologous nucleic acids. Primers and
CC probes derived from the RBP-7 nucleotide sequence (e.g. AAZ87035-287099)
CC are useful for DNA amplification and detection methods. RBP-7 biallelic
CC markers (see AAZ86993-287034) are useful for diagnosis of disease
CC related to alteration in the regulation or in the coding regions of the
CC RBP-7 gene and for prognosis/diagnosis of an eventual treatment with
CC therapeutic agents, especially agents acting on pathologies involving
CC abnormal cell proliferation and/or differentiation, these include
CC thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
CC including breast cancer, sarcomas and other neoplasms, bladder cancer,
CC colon cancer, lung cancer, prostate cancer, various leukaemias, and
CC lymphomas. RBP-7 antibodies are useful as diagnostic agents.
XX
SO Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other:
XX
Query Match 29.5%; Score 35.4; DB 21; Length 162450;
Best Local Similarity 61.3%; Pred. No. 0.36;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
OY 26 agagcagaccccttggaagaagaatactaagttattccctgactctctatttttaa 85
DB 82403 atagatgaactgtgagcagcagctgctggttgaatcctgctgcactctctg 82462
OY 86 ctaccatcttgccaatgttgcttaagctttt 118
DB 82463 ctgtgactcttggaatgtgtaacttaactttt 82495
RESULT 8
AAC69140
ID AAC69140 standard; DNA; 7052 BP.
XX
XX AAC69140;
XX
XX 29-JAN-2001 (first entry)
DE
XX Human ABC1 gene exons 23-28.
XX
XX Human ABC1 cholesterol transporter; chromosome 9q31;
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KW cardiovascular disease; coronary artery disease; coronary restenosis;
KW cerebrovascular disease; peripheral vascular disease;
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
XX prognosis; prophylaxis; drug screening; transgenic animal; ds.
XX
XX Homo sapiens.
OS
XX WO200055318-A2.
XX
XX 21-SEP-2000.
PD
XX 15-MAR-2000; 2000WO-1B00532.
PF
XX 15-MAR-1999; 99US-0124702.
PR 08-JUN-1999; 99US-0138048.
XX 17-JUN-1999; 99US-0139600.
PR 01-SEP-1999; 99US-0151977.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON BIORESEARCH INC.
XX
XX Hayden MR, Wilson AR, Pimstone SN;
PI
XX WPI: 2000-587528/55.
DR
XX

PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI: 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
PT cancer
XX
PS Claim 1; SEQ ID NO 78; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes having a sequence taken from 536 (actually 533 since
CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms and also to be used in an
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC and/or therapy of existing diseases or the predisposition to specific
CC diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes. Sequences with even numbered Seq ID numbers are the
CC complementary sequence of the corresponding odd numbered sequence (e.g.
CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
CC is missing).
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 14537 BP; 3628 A; 495 C; 3778 G; 6636 T; 0 other;
XX
Query Match 29.3%; Score 35.2; DB 22; Length 14537;
Best Local Similarity 60.4%; Pred. No. 0.2;
Matches 58; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 20 atagaagagcagacctgggagcagaataatcttaactgactgcctgactt 79
DB 1336 ATTCATAAACTCTAACCTTATTAACCTTAACCTTAATTAATCTTAACCCGCTACT 1277
QY 80 tattaactaacatcttgcacatgcttcttaagct 115
DB 1276 TATTAAACATATAACCTTAATAATTAATTAATCTTAACT 1241
RESULT 11
AAK65581
ID AAK65581 standard; DNA; 56632 BP.
XX
AC AAK65581;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:20393.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX

XX Homo sapiens.
OS
XX
PN MO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.

PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX WPI; 2001-244356/25.
XX
XX
XX Treating a lower than normal high density lipoprotein-cholesterol
PR (HDL-C) level, a higher than normal triglyceride level, or a
PR cardiovascular disease, by administering a compound that modulates LXR-
PR or RXR-mediated transcriptional activity -
XX
XX Claim 8; Fig 1; 317pp; English.
XX
XX The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.
XX
XX Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
S0
Query Match 29.3%; Score 35.2; DB 22; Length 183999;
Best Local Similarity 62.5%; Pred. No. 0.43;
Matches 55; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 32 gacattggagcaagaatctaatctgactctgctatttacttaacc 91
Db 145152 gggaggttgagcacaagagcagtggaatccgactctgactattgctatat 145211
QY 92 atcttgccaatgttgcttaagctttt 119
Db 145212 gaccttgggcaagctgctagtctctc 145239
RESULT 13
AAL13265
ID AAL13265 standard; cDNA; 267 BP.
XX
XX AAL13265;
XX
XX 07-DEC-2001 (first entry)
XX
XX Human breast cancer expressed polynucleotide 5722.
DE Human breast cancer; cell marker; cytostatic; ss.
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
KM
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX 19-JUL-2001.
PD
XX
XX 10-JAN-2001; 2001WO-US00798.
PF
XX
XX 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192059.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -

XX
PS Claim 1; Page 1029; 3695pp; English.
XX
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
XX Sequence 267 BP; 77 A; 46 C; 51 G; 90 T; 3 other;
S0
Query Match 29.0%; Score 34.8; DB 22; Length 267;
Best Local Similarity 64.6%; Pred. No. 0.08;
Matches 51; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 17 ggcataagaagagcagcactggagcaagaatatctaagtttaactgactctgt 76
Db 31 gggaaaaaaatcgtggaatttgagagacaacaataccagntaatactcacttgc 90
QY 77 attacttaactaacatct 95
Db 91 actacttaactaatattct 109
RESULT 14
AAL22135
ID AAL22135 standard; cDNA; 305 BP.
XX
XX AAL22135;
XX
XX 07-DEC-2001 (first entry)
XX
XX Human breast cancer expressed polynucleotide 14592.
DE Human breast cancer; cell marker; cytostatic; ss.
XX
XX Human; breast cancer; cell marker; cytostatic; ss.
KM
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX 19-JUL-2001.
PD
XX
XX 10-JAN-2001; 2001WO-US00798.
PF
XX
XX 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192059.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer -
PS Claim 1; Page 2627; 3695pp; English.
XX
XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and

08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
DR WPI: 2001-451937/48.
XX
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX
PS
PS
XX
XX
CC Example 2; SEQ ID NO 2665; 781bp + Sequence Listing; English.
CC
CC The invention relates to novel genes (ALJ34669-ALJ37666) and proteins
CC (ABR03087-ABR04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX
SQ Sequence 4171 BP; 1079 A; 1015 C; 1025 G; 1052 T; 0 other;

Query Match 28.5%; Score 34.2; DB 22; Length 4171;

Best Local Similarity 60.0%; Pred. No. 0.29;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 24 aaagagcagagccttggagcagaataatcctaagttaattcctgactctgtattatt 83
Db 997 aagcacagagccttggagcagaataatcctaagttaattcctgactctgtattatt 1056
QY 84 aactaacatcttgcacatgttgcattgaacttt 118
Db 1057 agcttctgacacttgcacagcagcgttaagcctgt 1091

Search completed: September 7, 2002, 18:40:27
Job time: 29921 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:55 ; Search time 12179.2 Seconds
(without alignments)
206.186 Million cell updates/sec

Title: US-09-834-291-1_COPY_337_456
Perfect score: 120
Sequence: 1 taagggaaggaggtatgca.....aatgttgcttaagcttttt 120

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	120	100.0	2344	9	HSCD955FR	X87625 H. sapiens C
2	120	100.0	2827	6	AX026092	AX026092 Sequence
3	120	100.0	3212	6	AX026089	AX026089 Sequence
4	120	100.0	187313	4	AL157394	AL157394 Human DNA
5	49.6	41.3	131286	4	AB053451	AB053451 Sus scrofa
6	47.6	39.7	166847	9	AC073148	AC073148 Human sapi
7	47.2	39.3	128765	9	AL1355852	AL1355852 Human sapi
8	45.8	38.2	162043	2	AC018803	AC018803 Homo sapi
9	45.8	38.2	166076	2	AC090587	AC090587 Homo sapi
10	45.8	38.2	166496	2	AC090804	AC090804 Homo sapi
11	44.8	37.3	157790	9	AL133413	AL133413 Human DNA
12	43.8	36.5	57449	9	AL1390768	AL1390768 Human DNA
13	43.8	36.5	172516	2	AL136384	AL136384 Homo sapi
14	43.6	36.3	131427	9	HS37J18	Z98747 Human DNA
15	43.6	36.3	157185	9	AC064798	AC064798 Homo sapi
16	43.2	36.0	101339	9	AL592226	AL592226 Human DNA
17	43.2	36.0	152754	9	AC096552	AC096552 Homo sapi
18	43.2	36.0	160071	2	AC016926	AC016926 Homo sapi
19	43.2	36.0	169332	2	AC068631	AC068631 Homo sapi
20	42.8	35.7	86156	2	AL162262	AL162262 Homo sapi
21	42.8	35.7	136649	9	HSD635E8	AL110502 Human DNA
22	42.4	35.3	170677	2	AL138932	AL138932 Homo sapi
23	42.4	35.3	175386	9	AL138930	AL138930 Human DNA
24	42.4	35.3	176698	2	AL355996	AL355996 Homo sapi
25	42.4	35.3	179614	2	AC012471	AC012471 Homo sapi
26	42.2	35.2	63722	2	AC103740	AC103740 Homo sapi
27	42.2	35.2	149042	2	AC016410	AC016410 Homo sapi
28	42.2	35.2	187005	2	AC024309	AC024309 Homo sapi
29	41.6	34.7	143899	2	AC013606	AC013606 Homo sapi
30	41.6	34.7	165434	2	AC087505	AC087505 Homo sapi
31	41.6	34.7	187566	2	AC015685	AC015685 Homo sapi
32	41.6	34.7	189876	2	AP000781	AP000781 Homo sapi
33	41.6	34.7	200841	2	AP002893	AP002893 Homo sapi
34	41.4	34.5	88323	9	AL162423	AL162423 Human DNA
35	41.4	34.5	108373	9	AL358034	AL358034 Human DNA
36	41.4	34.5	174852	2	AC010195	AC010195 Homo sapi
37	41.2	34.3	179966	2	AC023247	AC023247 Homo sapi
38	40.6	33.8	71794	2	AC023647	AC023647 Homo sapi
39	40.6	33.8	71794	2	AC023647	AC023647 Homo sapi
40	40.6	33.8	131329	9	AC004873	AC004873 Homo sapi
41	40.6	33.8	153218	2	AC015920	AC015920 Homo sapi
42	40.6	33.8	160254	9	AC007763	AC007763 Homo sapi
43	40.6	33.8	169243	9	HS11123D4	AL049691 Human DNA
44	40.6	33.8	170867	9	AC068295	AC068295 Homo sapi
45	40.6	33.8	173010	9	CNS01DSU	AL122013 Human chr

ALIGNMENTS

RESULT 1	HSCD955FR	2344 bp	DNA	Linear	PRI 05-FEB-1997
LOCUS	HSCD955FR				
DEFINITION	H. sapiens CD95 gene 5' flanking region.				
ACCESSION	X87625				
VERSION	X87625.1 GI:902311				
KEYWORDS	beta interferon; CD95 gene; silencer.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 2344) Rudert, F., Visser, E., Forbes, L., Lindridge, E., Wang, Y. and Watson, J.				
TITLE	Identification of a silencer, enhancer, and basal promoter region in the human CD95 (Fas/APO-1) gene				
JOURNAL	DNA Cell Biol. 14 (11), 931-937 (1995)				
MEDLINE	96069539				
REFERENCE	2 (bases 1 to 2344)				
AUTHORS	Rudert, F.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-MAY-1995) F.H. Rudert, Genesis Research & Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND				

COMMENT Overlaps with X81335, & X82279-X82286.
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Location/Qualifiers
1. .2344
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/germline
/tissue_type="placenta"
/map="q24.1"
564. .1337
misc_signal
/note="silencer"
717. .801
misc_signal
/note="beta interferon silencer B motifs"
complement(1237. .1244)
misc_signal
/note="lysosome silencer 1"
1338. .1919
enhancer
1920. .2344
promoter
/note="basal promoter"
BASE COUNT 637 a 546 c 511 g 650 t
ORIGIN

Query Match 100.0%; Score 120; DB 9; Length 2344;
Best Local Similarity 100.0%; Pred. No. 4.4e-25;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taagggaagggggtatgcatagagaagcagaccttgggagcaagaatatacttaagttt 60
Db 454 TAGGGGAAGGGGGTATGCGATAGAAAGACGACCTTGGGAGCAGAAATATCTAAGTTT 513

QY 61 aattccgactctgctattatataactaacacatttgcgaatgttgccttaagcttttt 120
Db 514 AATTCCGACTCTGCTATTATTACTAACCAATCTTGGCCAAATGTTGCTTAAGCTTTT 573

RESULT 2
AX026092 2827 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION Sequence 4 from Patent DE19847779.
ACCESSION AX026092.1 GI:10187523
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2827)
Muller-Schilling, M., Kramer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 4 03-FEB-2000;
JOURNAL DEUTSCHES KREBSFORSCH (DE)
FEATURES
Source
1. .2827
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 728 a 676 c 657 g 766 t
ORIGIN

Query Match 100.0%; Score 120; DB 6; Length 2827;
Best Local Similarity 100.0%; Pred. No. 4.4e-25;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taagggaagggggtatgcatagagaagcagaccttgggagcaagaatatacttaagttt 60
Db 337 TAGGGGAAGGGGGTATGCGATAGAAAGACGACCTTGGGAGCAGAAATATCTAAGTTT 396

QY 61 aattccgactctgctattatataactaacacatttgcgaatgttgccttaagcttttt 120
Db 397 AATTCCGACTCTGCTATTATTACTAACCAATCTTGGCCAAATGTTGCTTAAGCTTTT 456

RESULT 3
AX026089 3212 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION Sequence 1 from Patent DE19847779.
ACCESSION AX026089.1 GI:10187520
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3212)
Muller-Schilling, M., Kramer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 1 03-FEB-2000;
JOURNAL DEUTSCHES KREBSFORSCH (DE)
FEATURES
Source
1. .3212
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 778 a 784 c 809 g 841 t
ORIGIN

Query Match 100.0%; Score 120; DB 6; Length 3212;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taagggaagggggtatgcatagagaagcagaccttgggagcaagaatatacttaagttt 60
Db 337 TAGGGGAAGGGGGTATGCGATAGAAAGACGACCTTGGGAGCAGAAATATCTAAGTTT 396

QY 61 aattccgactctgctattatataactaacacatttgcgaatgttgccttaagcttttt 120
Db 397 AATTCCGACTCTGCTATTATTACTAACCAATCTTGGCCAAATGTTGCTTAAGCTTTT 456

RESULT 4
AL157394 187313 bp DNA linear PRI 22-AUG-2001
LOCUS
DEFINITION Human DNA sequence from clone RP11-395019 on chromosome 10,
complete sequence.
ACCESSION AL157394
VERSION AL157394.15 GI:15384622
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 187313)
Blakey, S.
Direct Submission
Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP

database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/NGP/Chr10>
 RPI1-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6

This sequence is the entire insert of clone RPI1-399019. The true left end of clone RPI1-496H23 is at 166408 in this sequence. The true right end of clone RPI1-30415 is at 18704 in this sequence.

FEATURES

source
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 /db_xref="taxon:9606"
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 100157..100198
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 105808..105972
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 105973..105989
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 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3.3e-25;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taagggaagggggtatgcatagaagaagacgcttgaggagaagaataatcagctt 60

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QY 61 aattcctgactcgtctatttattactaacatcttgcgaatgtgcttaagctttt 120

Db 142365 AATTCCGACTCTGCTATTATTAACCTACCATCTTGCCATGTTGCTTAAGCTTTT 142424

RESULT 5

AB053451 131286 bp DNA linear MAM 05-JAN-2002

LOCUS AB053451 131286 bp DNA constant regions and joining segments of T cell receptor alpha/delta chain.

ACCESSION AB053451

VERSION AB053451.1 GI:18147392

KEYWORDS Sus scrofa DNA.

SOURCE Sus scrofa.

ORGANISM Sus scrofa; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (sites) Thome, A., Saalmueller, A. and Pfaff, E.

AUTHORS Molecular cloning of porcine T cell receptor alpha, beta, gamma and delta chains using polymerase chain reaction fragments of the constant regions

TITLE Eur. J. Immunol. 23 (5), 1005-1010 (1993)

JOURNAL 93238851

MEDLINE 2 (sites) Yang, Y.G., Ohta, S., Yamada, S., Shimizu, M. and Takagaki, Y.

AUTHORS Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old pig

JOURNAL J. Immunol. 155 (4), 1981-1993 (1995)

MEDLINE 3 (sites) Uenishi, H.

AUTHORS Complete sequence of segments of joining and constant region of

JOURNAL porcine TCR gene alpha/delta locus
 REFERENCE 4 (bases 1 to 131286)
 AUTHORS Uenishi, H.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2001) Hirohide Uenishi, National Institute of Animal Health, MAF, Department of Animal Breeding and Genetics, P.O. Box 5, Tsukuba 305-0901, Japan (E-mail: huenishi@affrc.go.jp, Tel: 81-298-38-8627, Fax: 81-298-38-8793)

FEATURES

source

1..131286

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/db_xref="taxon:9823"

/chromosome="7"

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misc_signal 1491..1497

J_segment 1498..1551

CDS <1498..>1551

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misc_signal 1491..1497

J_segment 1498..1551

CDS <1498..>1551

misc_signal 1498..1551

misc_signal 1491..1497

J_segment 1498..1551

CDS <1498..>1551

misc_signal 1498..1551

misc_signal 1491..1497

J_segment 1498..1551

CDS <1498..>1551

misc_signal 1498..1551

misc_signal 1491..1497

J_segment 1498..1551

CDS <1498..>1551

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misc_signal 1491..1497

J_segment 1498..1551

CDS <1498..>1551

misc_signal 1498..1551

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 /translation="TLMAHPIFGNGTQLNVEP"
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          VAKTSEICEPEQVQAKVMMSVTYLGFRMLFAKSVAVNFLTAKILFF"
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          /db_xref="GI:18147397"
          /translation="SQPNKSPSYFVAKNGTNAVCLYKDFPKDKIKISLESSKITTEYD
          PAIVSPTRKISAVKLGOYGDPAVTCVSQHDQDTLHSDAFEEKNSSETPKPKESSEN
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          14849..14914
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          /number=2
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          /db_xref="GI:18147397"
          /translation="SQPNKSPSYFVAKNGTNAVCLYKDFPKDKIKISLESSKITTEYD
          PAIVSPTRKISAVKLGOYGDPAVTCVSQHDQDTLHSDAFEEKNSSETPKPKESSEN
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          15573..15686
          /note="putative"
          /citation=[1]
          /number=3
          /product="TCR delta chain constant region"
          15687..16845
          /note="TCR delta chain constant region"
          /protein_id="BAB83180.1"
          /db_xref="GI:18147397"
          /translation="SQPNKSPSYFVAKNGTNAVCLYKDFPKDKIKISLESSKITTEYD
          PAIVSPTRKISAVKLGOYGDPAVTCVSQHDQDTLHSDAFEEKNSSETPKPKESSEN
          VAKTSEICEPEQVQAKVMMSVTYLGFRMLFAKSVAVNFLTAKILFF"
          16846..>17784
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          /protein_id="BAB83180.1"
          /db_xref="GI:18147397"
          /translation="SQPNKSPSYFVAKNGTNAVCLYKDFPKDKIKISLESSKITTEYD
          PAIVSPTRKISAVKLGOYGDPAVTCVSQHDQDTLHSDAFEEKNSSETPKPKESSEN
          VAKTSEICEPEQVQAKVMMSVTYLGFRMLFAKSVAVNFLTAKILFF"
          17785..18488
          /note="putative"
          /citation=[1]
          /number=4
          /product="TCR delta chain constant region"
          18489..19550
          /note="putative"
          /number=1
          /product="TCR delta-5 chain variable region"
          complement(join(<20205..20512,20767..20800))
          /standard_name="TCR delta-5 chain variable region"
          complement(20513..20766)
          /standard_name="TCR delta-5 chain variable region"
          /note="putative"
          /number=1
          20647..20652

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exon      /note="putative"
          complement(20767..>20875)
          /note="putative"
          reverse transcriptional orientation"
          /number=2
          /product="TCR delta-5 chain variable region"
          20793..27801
          /note="putative recombination recognition sequence"
          27802..27816
          /note="putative recombination recognition sequence"
          27817..27880
          /note="putative recombination recognition sequence"
          27881..>27886
          /standard_name="possible TCRJ 61 gene segment"
          /standard_name="possible TCRJ 61 gene segment"
          /note="putative"
          /codon_start=3
          /protein_id="BAB83182.1"
          /db_xref="GI:18147399"
          /translation="KGVNRKLTFGAKTRGILKL"
          28789..28797
          /note="putative recombination recognition sequence"
          28800..28816
          /note="putative recombination recognition sequence"
          <28817..>28873
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          /note="putative"
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Query Match      41.3%; Score 49.6; DB 4; Length 131286;
Best Local Similarity 67.3%; Pred. No. 0.0016;
Matches 70; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY      16  tggcatagaagagagagaccttgggagcaagaatataatcctgactcgc 75
Db      16474  TTGCATTAAGAGAGACACCTAGCAATCAGAGAGCAAGCTTATCTGACTTGT 16533

QY      76  tattataactaacaccatcttgcacatgttgcttaagctttt 119
Db      16534  CACTACTACTGCTGTACCTTAGCCAGGTGCTTACTCTCT 16577

RESULT      6
AC073148/c  166847 bp  DNA  linear  PRI 03-JAN-2002
LOCUS      AC073148
DEFINITION Homo sapiens chromosome 7 clone RP11-801B4, complete sequence.
ACCESSION  AC073148
VERSION    AC073148.7  GI:11415226
KEYWORDS   HTG.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE   1  (bases 1 to 166847)
AUTHORS    Waterston,R.H.
TITLE      The sequence of Homo sapiens clone
JOURNAL    Unpublished
REFERENCE   2  (bases 1 to 166847)
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (08-JUN-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            3  (bases 1 to 166847)
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (29-NOV-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            4  (bases 1 to 166847)
AUTHORS    Waterston,R.
TITLE      Direct Submission
JOURNAL    Submitted (09-MAY-2001) Department of Genetics, Washington

```


REFERENCE 5 (bases 1 to 166847)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On Nov 29, 2000 this sequence version replaced g1:1128450.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@wustl.wustl.edu
Project Information
Center project name: H_NH0801B04

----- Location/Qualifiers -----
1..166847
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/clone="RP11-801B4"
/clone="RP11-801B4"

BASE COUNT 48276 a 31805 c 32820 g 53946 t
ORIGIN

Query Match 39.7%; Score 47.6; DB 9; Length 166847;
Best Local Similarity 69.1%; Pred. No. 0.0006;
Matches 65; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 25 aagagcaggacacctggagcagaagatactcaagtaactctgactctgtattat 84
DB 10828 AAGAGCATGATTACAGAGCCAGATACCTCAGTTGATCTCTACTACTATTATTA 10769
QY 85 actaccatcttgccaatgtgtcctaagctttt 118
DB 10768 GCTACCTAATCTGGCGACGTTCTTTACCTCT 10735

RESULT 7
LOCUS AL355852 128765 bp DNA linear PRI 09-MAR-2001
DEFINITION Human DNA sequence from clone RP11-403E24 on chromosome X, complete sequence.
ACCESSION AL355852
VERSION AL355852.23 GI:13274693
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 128765)
HeatP.
Direct Submission
Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, UK
Requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced g1:12964290.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGF/ChrX>
RP11-403E24 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-403E24 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-403E24 is at 1 in this sequence. The true left end of clone RP11-284B18 is at 128666 in this sequence. The true right end of clone RP11-33N11 is at 69175 in this sequence.

----- Location/Qualifiers -----
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-403E24"
/clone="lib-RP11-11.2"
1..5927
/note="L1PA7 repeat: matches 251..6141 of consensus"
6313..6419
/note="MER91C repeat: matches 15..139 of consensus"
6875..7885
/note="L1MC4 repeat: matches 7269..7643 of consensus"
7784..7892
/note="MIR repeat: matches 20..130 of consensus"
9981..10022
/note="21 copies 2 mer aa 81% conserved"
11037..11084
/note="MIR repeat: matches 100..145 of consensus"
11410..11615
/note="MIR repeat: matches 12..219 of consensus"
11683..11714
/note="MIR repeat: matches 12..219 of consensus"
11715..11918
/note="16 copies 2 mer ct 100% conserved"
12338..12441
/note="L2 repeat: matches 2513..2708 of consensus"
12338..12441
/note="MIR repeat: matches 45..147 of consensus"
complement(12973..13643)
/note="match: STS: Em:HSC63F11"
13218..13465
/note="MIR repeat: matches 13..262 of consensus"
13474..13595
/note="L2 repeat: matches 2591..2719 of consensus"
13854..14060
/note="L2 repeat: matches 2060..2281 of consensus"
14358..14451
/note="L2 repeat: matches 2418..2511 of consensus"
14559..14592
/note="17 copies 2 mer ct 94% conserved"
14817..15016
/note="MIR repeat: matches 8..216 of consensus"
16127..16404
/note="MIR repeat: matches 5..262 of consensus"
16822..16881
/note="L2 repeat: matches 2644..2705 of consensus"
16971..17060
/note="L2 repeat: matches 2589..2748 of consensus"
17552..17815
/note="match: STS: Em:G05256"
17870..18109
/note="L2 repeat: matches 2252..2519 of consensus"
18562..18822
/note="L2 repeat: matches 1630..1882 of consensus"
19119..19214

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repeat_region	/note="L2 repeat: matches 2042. .2135 of consensus" 20593. 21070
repeat_region	/note="LIME1 repeat: matches 5558. .6033 of consensus" 21074. .21182
repeat_region	/note="LIPAI1 repeat: matches 6068. .6184 of consensus" 21201. .22910
repeat_region	/note="LIME1 repeat: matches 3839. .5546 of consensus" 22919. .28163
repeat_region	/note="LIPAI3 repeat: matches 902. .6146 of consensus" 28160. .28375
repeat_region	/note="LIPAI3 repeat: matches 569. .777 of consensus" 28374. .29301
repeat_region	/note="LINS repeat: matches 5219. .6146 of consensus" 29302. .29635
repeat_region	/note="LINS repeat: matches 4877. .5210 of consensus" 29629. .30212
repeat_region	/note="LIP repeat: matches 2. .595 of consensus" 30310. .30395
repeat_region	/note="LIMB4 repeat: matches 6095. .6180 of consensus" 30310. .31074
repeat_region	/note="LIPAI3 repeat: matches 5476. .6156 of consensus" 31086. .35151
repeat_region	/note="LIPAI1 repeat: matches 2107. .6164 of consensus" 35143. .35252
repeat_region	/note="LIP repeat: matches 3663. .3772 of consensus" 35265. .35365
repeat_region	/note="LIMAI3 repeat: matches 6203. .6304 of consensus" 35361. .37144
repeat_region	/note="LIMAI1 repeat: matches 4262. .6079 of consensus" 37144. .40022
repeat_region	/note="LIMAT repeat: matches 3291. .6278 of consensus" 40103. .41274
repeat_region	/note="LIM4 repeat: matches 2234. .3477 of consensus" 41274. .41312
repeat_region	/note="LIMEC repeat: matches 2253. .2291 of consensus" 41313. .41618
repeat_region	/note="LIMX repeat: matches 2. .305 of consensus" 41619. .42194
repeat_region	/note="LIMEC repeat: matches 2012. .2254 of consensus" 42212. .42343
repeat_region	/note="L1 repeat: matches 3217. .3348 of consensus" 42345. .42525
repeat_region	/note="LIM4 repeat: matches 2508. .2689 of consensus" 42537. .42636
repeat_region	/note="L1 repeat: matches 3467. .3570 of consensus" 42648. .44277
repeat_region	/note="LIMB4 repeat: matches 4023. .5667 of consensus" 44280. .44483
repeat_region	/note="ALIV repeat: matches 2. .207 of consensus" 44561. .45101
repeat_region	/note="LIMB4 repeat: matches 5654. .6163 of consensus" 45484. .45849
repeat_region	/note="MER4A repeat: matches 1. .366 of consensus" 45983. .46045
repeat_region	/note="L2 repeat: matches 2572. .2634 of consensus" 46069. .51314
repeat_region	/note="LIPAI3 repeat: matches 900. .6146 of consensus" 51310. .52068
repeat_region	/note="LIPAI3 repeat: matches 2. .776 of consensus" 52097. .52180
repeat_region	/note="L2 repeat: matches 2668. .2750 of consensus" 52330. .52415
repeat_region	/note="L2 repeat: matches 2623. .2706 of consensus" 52646. .52878
repeat_region	/note="MIR repeat: matches 7. .261 of consensus" 53213. .53900
repeat_region	/note="L2 repeat: matches 1999. .2707 of consensus" 54715. .55084
repeat_region	/note="L2 repeat: matches 2364. .2750 of consensus" 55251. .55282
repeat_region	/note="S repeat: matches 1. .42 of consensus"

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repeat_region      55293..55623
                    /note="L1M4 repeat: matches 3719..4071 of consensus"
repeat_region      55831..58846
                    /note="L1P25 repeat: matches 3139..6143 of consensus"
repeat_region      61230..61450
                    /note="BURL repeat: matches 11069..11275 of consensus"
repeat_region      61467..61997
                    /note="L1P13 repeat: matches 5629..6155 of consensus"
repeat_region      62098..62298
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repeat_region      62913..63274
                    /note="THEIC repeat: matches 3..371 of consensus"
repeat_region      63277..64587
                    /note="THEIC-internal repeat: matches 314..1646 of
consensus"
repeat_region      64586..64689
                    /note="THEI-INTERNAL repeat: matches 694..791 of
consensus"
repeat_region      64696..65003
                    /note="THEIC-internal repeat: matches 4..309 of consensus"
repeat_region      65007..65373
                    /note="THEIC repeat: matches 1..371 of consensus"
repeat_region      65376..65571

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Query Match          39.3%; Score 47.2; DB 9; Length 128765;
Best Local Similarity 67.0%; Pred. No. 0.0008;
Matches    67; Conservative   0; Mismatches    33; Indels     0; Gaps      0;
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OY 21 tagaaagacgaacctgggagcaagaatactcagttaattccgcactgtatatt 80
 | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89270 TCGTAGAGACGACCACTTTTCAGCTAGACGTCTTGAAGGCCAATCCACTTCTCCTACT 89211

OY 81 attaacaccacatcttgcacaatgttgtttaagcttttt 120
 | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89210 ATTACTATGTGCACATTGAACAAGTGCTTTAACTTTTCTT 89171

RESULT	8
AC018803/c	
LOCUS	
DEFINITION	162043 bp DNA linear HTG_07-JUL-2000
ACCESSION	AC018803
VERSION	Homo sapiens chromosome 11 clone Rpl1-348A20, WORKING DRAFT
KEYWORDS	SEQUENCE, 23 unordered pieces.
SOURCE	AC018803.2 GI:7231004
ORGANISM	HTG; HTGS_PHASE1; HTGS_DRAFT. human. Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 162043)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 162043)
Waterston, R.H.
Direct Submission
Submitted (20-DEC-1999) Genome Sequencing Center, Washington

COMMENT

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H_NH0348A20
Summary Statistics
-----
Sequencing vector: plasmid: 29%
Chemistry: Dye-Primer ET; 71% of reads
Chemistry: Dye-terminator Big Dye; 29% of reads
Assembly program: Phrap; version 0.990319

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Consensus quality: 148994 bases at least Q40
Consensus quality: 153397 bases at least Q30
Consensus quality: 155868 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 159843; sum-of-contigs
Quality coverage: 3.23 in Q20 bases; agarose-fp
Quality coverage: 3.56 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1403: contig of 1403 bp in length
* 1404 1503: gap of unknown length
* 1504 3139: contig of 1636 bp in length
* 3140 3239: gap of unknown length
* 3240 4924: contig of 1685 bp in length
* 4925 5024: gap of unknown length
* 5025 7122: contig of 2098 bp in length
* 7123 7222: gap of unknown length
* 7223 9888: contig of 2766 bp in length
* 9889 10088: gap of unknown length
* 10089 12884: contig of 2796 bp in length
* 12885 15878: gap of unknown length
* 15879 15978: gap of unknown length
* 15979 21740: contig of 5762 bp in length
* 21741 26572: contig of 4732 bp in length
* 26573 30641: contig of 3969 bp in length
* 30642 30741: gap of unknown length
* 30742 35422: contig of 4681 bp in length
* 35423 35522: gap of unknown length
* 35523 40850: contig of 5328 bp in length
* 40851 40950: gap of unknown length
* 40951 45830: contig of 4880 bp in length
* 45831 45930: gap of unknown length
* 45931 50449: contig of 4519 bp in length
* 50450 50549: gap of unknown length
* 50550 56392: contig of 5843 bp in length
* 56393 56492: gap of unknown length
* 56493 63159: contig of 6667 bp in length
* 63160 63259: gap of unknown length
* 63260 69649: contig of 6390 bp in length
* 69650 69749: gap of unknown length
* 69750 77072: contig of 7323 bp in length
* 77073 77172: gap of unknown length
* 77173 89806: contig of 12634 bp in length
* 89807 89906: gap of unknown length
* 89907 103817: contig of 13911 bp in length
* 103818 103917: gap of unknown length
* 103918 117239: contig of 13322 bp in length
* 117240 117339: gap of unknown length
* 117340 139330: contig of 21991 bp in length
* 139331 139430: gap of unknown length
* 139431 162043: contig of 22613 bp in length.

Location/Qualifiers
1. 162043
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/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-348A20"
1. 1403
/note="assembly_name:Contig10"
1504. .3139
/note="assembly_name:Contig11"
3240. .4924
/note="assembly_name:Contig12"

misc_feature 5025. .7122
/note="assembly_name:Contig13"
misc_feature 7223. .9988
/note="assembly_name:Contig14"
misc_feature 10089. .12884
/note="assembly_name:Contig15
clone_end:77
vector_side:right"
misc_feature 12985. .15878
/note="assembly_name:Contig16"
misc_feature 15979. .21740
/note="assembly_name:Contig17"
misc_feature 21841. .26572
/note="assembly_name:Contig18"
misc_feature 26673. .30641
/note="assembly_name:Contig19"
misc_feature 30742. .35422
/note="assembly_name:Contig20"
misc_feature 35523. .40850
/note="assembly_name:Contig21"
misc_feature 40951. .45830
/note="assembly_name:Contig22"
misc_feature 45931. .50449
/note="assembly_name:Contig23"
misc_feature 50550. .56392
/note="assembly_name:Contig24"
misc_feature 56493. .63159
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misc_feature 63260. .69649
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misc_feature 69750. .77072
/note="assembly_name:Contig27"
misc_feature 77173. .89806
/note="assembly_name:Contig28"
misc_feature 89907. .103817
/note="assembly_name:Contig29"
misc_feature 103918. .117239
/note="assembly_name:Contig30"
misc_feature 117340. .139330
/note="assembly_name:Contig31"
misc_feature 139431. .162043
/note="assembly_name:Contig32"
BASE COUNT 45380 a 35428 c 35430 g 43508 t 2297 others
ORIGIN
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Best Local Similarity 64.8%; Pred. No. 0.002;
Matches 68; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 15 atggcatagaagaagcagccttggagcagaatacttaagtttaattccgactctg 74
||| ||||| || ||| ||| ||||| ||| ||||| |||
DB 145886 ATGTGTAGAACACATTAACCTGTGGCCAGACAACTCAAGGTCAAACTGATTGTTG 145827
QY 75 ctattataactaacacatcttgcacatgttgcctaagctttt 119
||||| ||||| ||| ||| ||| ||||| ||| |||
DB 145826 CATTTCCTAGCTGTACCTGGAATAAATGCTTAACCTCTGT 145782
RESULT 9
AC090587 166076 bp DNA linear HTG 21-JUN-2001
LOCUS Homo sapiens chromosome 11 clone RP11-348A20 map 11, WORKING DRAFT
DEFINITION
SEQUENCE, 18 unordered pieces.
ACCESSION AC090587
VERSION AC090587.3 GI:14971229
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 166076)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE
JOURNAL
REFERENCE
AUTHORS

Homo sapiens chromosome 11, clone RP11-348A20

Unpublished
2 (bases 1 to 166076)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Batta, N., Bastien, V., Boguslavsky, L., Bouckhagalter, B., Brown, A., Camarata, J., Campoliano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Garday, S., Glade, S., Goyette, M., Graham, L., Grand-Pierre, N., Haas, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karata, A., Laroque, K., Lamazares, R., Landers, T., Lehoucq, N., Levine, R., Liu, G., Maclean, C., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McKean, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Sougnier, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testfay, S., Theodore, J., Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL

Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 20, 2001 this sequence version replaced gi:14210549.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: 348_A-20

Center clone name: 111802

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 160051 bases at least Q40

Consensus quality: 162378 bases at least Q30

Consensus quality: 163489 bases at least Q20

Insert size: 164000; agarose-ff

Quality coverage: 8.2 in Q20 bases; sum-of-coverage

Quality coverage: 8.2 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 5708: contig of 5708 bp in length
* 5709 5808: gap of 100 bp
* 5809 6864: contig of 1056 bp in length
* 6865 6964: gap of 100 bp
* 6965 8333: contig of 1369 bp in length
* 8334 8433: gap of 100 bp
* 8434 10150: contig of 1717 bp in length
* 10151 10250: gap of 100 bp
* 10251 11856: contig of 1606 bp in length
* 11857 11956: gap of 100 bp
* 11957 13685: contig of 1729 bp in length
* 13686 13785: gap of 100 bp
* 13786 16873: contig of 3087 bp in length
* 16873 16972: gap of 100 bp

FEATURES
source

* 16973 20146: contig of 3174 bp in length
* 20147 20246: gap of 100 bp
* 20247 53285: contig of 33039 bp in length
* 53286 53385: gap of 100 bp
* 53386 56431: contig of 3046 bp in length
* 56432 56531: gap of 100 bp
* 56532 64713: contig of 8182 bp in length
* 64714 64813: gap of 100 bp
* 64814 72676: contig of 7863 bp in length
* 72677 72776: gap of 100 bp
* 72777 87626: contig of 14850 bp in length
* 87627 87726: gap of 100 bp
* 87727 102250: contig of 14524 bp in length
* 102251 102350: gap of 100 bp
* 102351 114827: contig of 12477 bp in length
* 114828 114927: gap of 100 bp
* 114928 129464: contig of 14537 bp in length
* 129465 129564: gap of 100 bp
* 129565 163190: contig of 33626 bp in length
* 163191 163290: gap of 100 bp
* 163291 165076: contig of 2786 bp in length.
Location/Qualifiers
1. 166076

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-348A20"
/clone_11p="RPC1-11 Human Male BAC"
1. 5708
/note="assembly-fragment
clone_end:SP6
vector_side:left"

misc_feature
5809..6864
/note="assembly-fragment"
misc_feature
6965..8333
/note="assembly-fragment"
misc_feature
8434..10150
/note="assembly-fragment"
misc_feature
10251..11856
/note="assembly-fragment"
misc_feature
11957..13685
/note="assembly-fragment"
misc_feature
13786..16872
/note="assembly-fragment"
misc_feature
16973..20146
/note="assembly-fragment"
misc_feature
20247..53285
/note="assembly-fragment"
misc_feature
53386..56431
/note="assembly-fragment"
misc_feature
56532..64713
/note="assembly-fragment"
misc_feature
64814..72676
/note="assembly-fragment"
misc_feature
72777..87626
/note="assembly-fragment"
misc_feature
87727..102250
/note="assembly-fragment"
misc_feature
102351..114827
/note="assembly-fragment"
misc_feature
114928..129464
/note="assembly-fragment"
misc_feature
129565..163190
/note="assembly-fragment"
misc_feature
163291..165076
/note="assembly-fragment
clone_end:T7
vector_side:right"

BASE COUNT 47135 a 36452 c 36434 g 44341 t 1714 others
ORIGIN

9934.11-34.2. Contains an MTND3 (mitochondrial NADH dehydrogenase 3) pseudogene, STSs and GSSs, complete sequence.
AL133413
AL133413.5 GI:6967346
HTG: MTND3.
human.
human sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 157790)
Lloyd,D.
Direct Submission
Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Feb 11, 2000 this sequence version replaced gi:6966862.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequencing criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unSURE' feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
EM: EMBL; SW: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C-elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-54K22 is from the library RPCR-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACE3.6
This sequence is the entire insert of clone RP11-54K22.

FEATURES
source
Location/Qualifiers
1..157790
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="g34.11-34.2"
/clone="RP11-54K22"
/clone.lib="RPC1-11.1"
1..576
/note="match: GSS: Em:AQ079263"
12..400
/note="match: GSS: Em:AQ083232
match: STS: Em:G53956"
17..242
/note="match: GSS: Em:B86764"
51..593
/note="match: GSS: Em:B89369"
51..397
/note="match: GSS: Em:B85038"
380..507
/note="MIR repeat: matches 56..192 of consensus"
566..630
/note="MIR repeat: matches 209..253 of consensus"
2127..2232
/note="MIR repeat: matches 2..120 of consensus"
2368..2510
/note="MIR repeat: matches 14..162 of consensus"
2856..2919
/note="MIR repeat: matches 45..112 of consensus"
2957..3102
/note="LIM8 repeat: matches 6140..6288 of consensus"

repeat_region
3096..3492
/note="LIM3 repeat: matches 5112..5529 of consensus"
3800..3904
/note="L2 repeat: matches 2393..2490 of consensus"
4484..4487
/note="TIGER2 repeat: matches 2334..2690 of consensus"
4908..5087
/note="AluSg/X repeat: matches 134..312 of consensus"
5108..5152
/note="TIGGER2 repeat: matches 1..45 of consensus"
6647..6994
/note="LIMB7 repeat: matches 5821..6167 of consensus"
8067..8217
/note="MER1C repeat: matches 268..421 of consensus"
8488..10072
/note="LIMD repeat: matches -1..1597 of consensus"
10112..10338
/note="MER2 repeat: matches 89..335 of consensus"
10339..10650
/note="AluYb8 repeat: matches 1..312 of consensus"
10651..10720
/note="MER2 repeat: matches 24..89 of consensus"
13021..13179
/note="MER45 repeat: matches 1..178 of consensus"
13830..13915
/note="LRR38 repeat: matches 1..87 of consensus"
13953..14420
/note="LRR38 repeat: matches 86..556 of consensus"
14730..14896
/note="LRR16C repeat: matches 208..371 of consensus"
16330..16929
/note="LIP3 repeat: matches 5547..6146 of consensus"
complement(17541..18049)
/note="match: GSS: Em:AQ677358"
complement(17569..17992)
/note="match: GSS: Em:AQ580536"
18024..18471
/note="LIMD2 repeat: matches 5842..6239 of consensus"
18472..18807
/note="MER1B repeat: matches 1..336 of consensus"
18808..18903
/note="LIMD2 repeat: matches 6239..6341 of consensus"
18901..19479
/note="LIME3A repeat: matches 5285..5895 of consensus"
19408..19879
/note="match: GSS: Em:AQ476746"
complement(19557..19992)
/note="match: GSS: Em:AQ177739"
21042..21464
/note="match: GSS: Em:AQ679820"
21067..21431
/note="match: GSS: Em:AQ409649"
21081..21546
/note="match: GSS: Em:AQ314497"
21180..21640
/note="match: GSS: Em:AQ228996"
21370..21677
/note="AluSg repeat: matches 1..304 of consensus"
21806..21845
/note="L2 repeat: matches 1781..1927 of consensus"
25755..25941
/note="L2 repeat: matches 1781..1927 of consensus"


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repeat_region /note="MLT1A2 repeat: matches 13. .114 of consensus"  
11392. .11770 /note="MLT1A2 repeat: matches 9. .374 of consensus"  
repeat_region 11771. .11884 /note="MLT1A2-internal repeat: matches 1. .113 of  
consensus"  
repeat_region 11895. .12082 /note="LIME1 repeat: matches 5964. .6164 of consensus"  
repeat_region 12140. .12436 /note="ALUv repeat: matches 1. .289 of consensus"  
repeat_region 12831. .13985 /note="ALUv repeat: matches 1. .289 of consensus"  
repeat_region 13993. .14056 /note="TRIGER1 repeat: matches 771. .1964 of consensus"  
repeat_region 14057. .14363 /note="L1PA16 repeat: matches 6093. .6157 of consensus"  
repeat_region 14364. .14376 /note="ALUv repeat: matches 1. .309 of consensus"  
repeat_region 14377. .14687 /note="L1PA16 repeat: matches 6081. .6093 of consensus"  
repeat_region 14688. .15421 /note="ALUx repeat: matches 1. .301 of consensus"  
repeat_region 15422. .15678 /note="L1PA16 repeat: matches 5329. .6081 of consensus"  
repeat_region 15679. .16039 /note="ALUx repeat: matches 8. .289 of consensus"  
repeat_region 16040. .16351 /note="L1PA16 repeat: matches 4960. .5329 of consensus"  
repeat_region 16352. .17086 /note="ALUx repeat: matches 1. .312 of consensus"  
repeat_region 17079. .17509 /note="L1PA16 repeat: matches 4252. .4960 of consensus"  
misc_feature /note="match: GSS: Em:AQ079766"  
repeat_region 17089. .17465 /note="TRIGER1 repeat: matches 1950. .2359 of consensus"  
repeat_region 17922. .18108 /note="ALUv repeat: matches 1. .185 of consensus"  
repeat_region 18784. .19104 /note="ALUv repeat: matches 1. .293 of consensus"  
repeat_region 19121. .20765 /note="L1PA2 repeat: matches 4493. .6146 of consensus"  
misc_feature 21580. .21989 /note="match: GSS: Em:B03931"  
repeat_region 23411. .23714 /note="ALUx repeat: matches 1. .302 of consensus"  
repeat_region 24111. .24395 /note="MER1A repeat: matches 1. .292 of consensus"  
repeat_region 24400. .24489 /note="L2 repeat: matches 1366. .2713 of consensus"  
repeat_region 25259. .25559 /note="ALUv repeat: matches 1. .299 of consensus"  
misc_feature complement(25341. .25695)  
repeat_region 26535. .26614 /note="match: GSS: Em:B40764"  
repeat_region 30408. .30779 /note="MIR repeat: matches 32. .112 of consensus"  
repeat_region 30869. .31357 /note="L1M9 repeat: matches 5959. .6303 of consensus"  
repeat_region 31376. .31910 /note="MER1A repeat: matches 1. .527 of consensus"  
repeat_region 31947. .33134 /note="MLT2D repeat: matches 42. .553 of consensus"  
misc_feature /note="L2 repeat: matches 1366. .2713 of consensus"  
complement(32984. .33714)  
repeat_region 33454. .33536 /note="match: GSS: Em:AQ377120"  
repeat_region 33537. .34804 /note="L1M10 repeat: matches 6240. .6319 of consensus"  
repeat_region 34805. .34877 /note="HSMAR2 repeat: matches 1. .1300 of consensus"  
repeat_region 35046. .41168 /note="L1M10 repeat: matches 6167. .6240 of consensus"  
repeat_region 41169. .41589 /note="L1PA2 repeat: matches 2. .6144 of consensus"  
  
repeat_region /note="LIMEC repeat: matches 1580. .2001 of consensus"  
41590. .41864 /note="ALUv repeat: matches 30. .304 of consensus"  
repeat_region 41865. .43166 /note="LIMEC repeat: matches 283. .1580 of consensus"  
repeat_region 43772. .43857 /note="L1 repeat: matches 1. .133 of consensus"  
repeat_region 44560. .44695 /note="L1 repeat: matches 1. .133 of consensus"  
misc_feature 44654. .44851 /note="match: GSS: Em:AQ451420"  
44655. .45072 /note="match: GSS: Em:AQ789501"  
45717. .45996 /note="L1 repeat: matches 3572. .3761 of consensus"  
repeat_region 46098. .46235 /note="L1M4 repeat: matches 3517. .3671 of consensus"  
repeat_region 46280. .46464 /note="L1 repeat: matches 3572. .3761 of consensus"  
repeat_region 46547. .46703 /note="L1 repeat: matches 3983. .4145 of consensus"  
repeat_region 47012. .47330 /note="LIME1 repeat: matches 4320. .4648 of consensus"  
repeat_region 47331. .47707 /note="LIME1 repeat: matches 1. .426 of consensus"  
repeat_region 47708. .48529 /note="LIME1 repeat: matches 4648. .5569 of consensus"  
repeat_region 48530. .48838 /note="LIME1 repeat: matches 3. .311 of consensus"  
repeat_region 48839. .49096 /note="LIME1 repeat: matches 5569. .5834 of consensus"  
repeat_region 49147. .49207 /note="LIME1 repeat: matches 25. .84 of consensus"  
repeat_region 49259. .49538 /note="MER2 repeat: matches 5833. .6099 of consensus"  
repeat_region 49359. .49823 /note="LIME1 repeat: matches 6. .287 of consensus"  
repeat_region 49824. .49884 /note="ALUv repeat: matches 1. .309 of consensus"  
misc_feature 50712. .51086 /note="LIME1 repeat: matches 6099. .6155 of consensus"  
repeat_region 50862. .50911 /note="match: STS: Em:G60437"  
repeat_region 51044. .51354 /note="L2 repeat: matches 1. .309 of consensus"  
repeat_region 51364. .51491 /note="L2 repeat: matches 2042. .2191 of consensus"  
repeat_region 51492. .51812 /note="L2 repeat: matches 1. .309 of consensus"  
  
Query Match 36.5%; Score 43.8; DB 9; Length 57449;  
Best Local Similarity 66.3%; Pred. No. 0.0084;  
Matches 63; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
  
OY 25 aagagcagccttggagcaagaataatgaatttaattcctgactctgtatlatra 84  
||||| ||| ||||| ||| ||| ||| ||||| ||| |||  
Db 3061 AAGAGGATGAGCTACAGCAAGCAAGCTTCCAAACGACGAGTCTGGTCTGCTACTTAAT 3002  
OY 85 actaacatcttgcgaatgttgccttaagctttt 119  
||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 3001 ACTTTCGACCTTGACACGATTAACTTGT 2967  
  
RESULT 13  
AL136384 172516 bp DNA linear HTG 26-Jul-2000  
LOCUS AL136384/c  
DEFINITION Homo sapiens chromosome 11 clone RP1-68P15 map p13-14.2. ***  
ACCESSION AL136384  
VERSION AL136384.8 GI:9542701  
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.  
SOURCE human.  
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 172516)
AUTHORS Hall, R.
TITLE Direct Submission
JOURNAL Submitted (25-Jul-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 27, 2000 this sequence version replaced gi:9501161.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: dj68P15
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ABI; 0% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Consensus quality: 155880 bases at least Q40
Consensus quality: 155942 bases at least Q30
Consensus quality: 155942 bases at least Q20
Insert size: 172416; sum-of-contigs
Insert size: 150759; 12.6% error; agarose-fp
Quality coverage: 0.00x in Q20 bases; sum-of-contigs Quality
coverage: 0.00x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 16300: contig of 16300 bp in length
* 16301 16400: gap of 100 bp
* 16401 172516: contig of 156116 bp in length.
* Location/Qualifiers
1..172516
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="p13-14.2"
/clone="RP1-68P15"
/clone_1lb="RPC1-1"
1..16300
/note="assembly_fragment:02897.0"
16401..172516
/note="assembly_fragment:02915.0"
BASE COUNT 56528 a 30286 c 30207 g 55395 t 100 others
ORIGIN
Query Match 36.5%; Score 43.8; DB 2; Length 172516;
Best Local Similarity 66.3%; Pred. No. 0.0078;
Matches 63; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 25 aagagcggagcttggagcagaataatcgaattatcctgctgcgtcattatata 84
|||||
DB 97986 AAGGAGTGACTCTAGCAGACTTCCAAACGACGCTGCTGCTACTTAATT 97927
|||||
QY 85 actaccatcttgcgaatgttgccttaagctttt 119
|||||
DB 97926 ACTTTGGACCTTGACACAAGTTAATTAACCTTGT 97892
|||||
RESULT 14 131427 bp DNA linear PRI 23-NOV-1999
HS37J18/c
LOCUS Human DNA sequence from clone 37J18 on chromosome 1p36.2-36.3.
DEFINITION

ACCESSION 298747
VERSION 298747.1 GI:3947813
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 131427)
AUTHORS Grafham, D.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Dec 2, 1998 this sequence version replaced gi:3925562.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence is the entire insert of clone 37J18. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre Chromosome 1
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
37J18 is from the library RPC11 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/VECTOR: PCYPAC2.
Location/Qualifiers
1..131427
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="p36.2-36.3"
/clone="RP1-37J18"
/clone_1lb="RPC1-1"
179..403
/note="L1M44 repeat: matches 6071..6295 of consensus"
423..518
/note="4 copies 24 mer 81% conserved"
521..1156
/note="212 copies 3 mer cac 80% conserved"
521..1168
/note="27 copies 24 mer 79% conserved"
563..1156
/note="9 copies 66 mer 82% conserved"
1544..1613
/note="MIR repeat: matches 141..210 of consensus"
2191..2709
/note="MIR repeat: matches 25..508 of consensus"
2834..3125
/note="AluX repeat: matches 1..294 of consensus"
3603..3882
/note="14 copies 20 mer 58% conserved"
3618..3899
/note="141 copies 2 mer cc 57% conserved"
3674..3784
/note="3 copies 37 mer 79% conserved"
3816..3926
/note="3 copies 37 mer 86% conserved"
3976..4031
/note="28 copies 2 mer tt 79% conserved"
4051..4141
/note="MIR repeat: matches 53..144 of consensus"
5386..5765
/note="MIRB repeat: matches 1..381 of consensus"

```

repeat_region 5862. .6059
/note="L1MB7 repeat: matches 5654. .5862 of consensus"
repeat_region 6060. 6116
/note="Charlie1 repeat: matches 2407. .2463 of consensus"
repeat_region 6180. .6476
/note="L1MB7 repeat: matches 5847. .6143 of consensus"
repeat_region 6535. .6856
/note="Charlie1 repeat: matches 2146. .2458 of consensus"
repeat_region 7077. .7103
/note="9 copies 3 mer tga 93% conserved"
repeat_region 7430. .7481
/note="13 copies 4 mer catl 77% conserved"
repeat_region 7536. .7712
/note="L1M4 repeat: matches 5086. .5272 of consensus"
repeat_region 7784. .7911
/note="L1M4 repeat: matches 5288. .5414 of consensus"
repeat_region 8170. .8475
/note="Alus9 repeat: matches 1. .308 of consensus"
repeat_region 8477. .8512
/note="12 copies 3 mer taa 83% conserved"
repeat_region 8517. .8646
/note="Alusx repeat: matches 6. .132 of consensus"
repeat_region 8647. .8960
/note="Alus9 repeat: matches 1. .313 of consensus"
repeat_region 8961. .9108
/note="Alusx repeat: matches 132. .289 of consensus"
repeat_region 10990. .11231
/note="MIR repeat: matches 2. .249 of consensus"
repeat_region 11467. .11756
/note="L2 repeat: matches 2359. .2625 of consensus"
repeat_region 12285. .12575
/note="Alusx repeat: matches 8. .309 of consensus"
misc_feature 12358. .12800
/note="match: GSS AQ0203924"
repeat_region 14049. .14489
/note="MER31B repeat: matches 1. .543 of consensus"
repeat_region 14734. .15230
/note="71 copies 7 mer gctgtgt 90% conserved"
repeat_region 14747. .15236
/note="7 copies 70 mer 91% conserved"
repeat_region 14748. .15237
/note="14 copies 35 mer 90% conserved"
repeat_region 14755. .15209
/note="5 copies 91 mer 93% conserved"
misc_feature 15124. .15428
/note="Tandem repeat: poor quality data over region"
repeat_region 15210. .15320
/note="3 copies 37 mer 78% conserved"
repeat_region 15230. .15684
/note="5 copies 91 mer 92% conserved"
misc_feature 15231
/note="Forced join in tandem repeat; gap sized by pUC clones and PAC PCR to be 1-200bp"
repeat_region 15312. .15661
/note="5 copies 70 mer 93% conserved"
repeat_region 15459. .15668
/note="6 copies 35 mer 91% conserved"
repeat_region 15681. .15827
/note="L2 repeat: matches 2538. .2685 of consensus"
repeat_region 15866. .16348
/note="MT1D repeat: matches 1. .504 of consensus"
repeat_region 16463. .16529
/note="L2 repeat: matches 2413. .2474 of consensus"
repeat_region 16974. .17269
/note="MER77 repeat: matches 5. .331 of consensus"
repeat_region 18532. .18555
/note="6 copies 4 mer aatg 100% conserved"
repeat_region 18712. .19007
/note="MT1E repeat: matches 249. .562 of consensus"
repeat_region 19100. .19140
/note="MT1E repeat: matches 72. .112 of consensus"
repeat_region 19854. .19922
/note="MIR repeat: matches 87. .163 of consensus"

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repeat_region	19928..19968	/note="MER5" repeat: matches 128..187 of consensus"
repeat_region	20239..20321	/note="MER53 repeat: matches 94..182 of consensus"
repeat_region	20256..20337	/note="MER53 repeat: matches 1..89 of consensus"
repeat_region	21622..21785	/note="MER63A repeat: matches 42..208 of consensus"
repeat_region	22083..22359	/note="12 repeat: matches 2416..2710 of consensus"
repeat_region	22441..22574	/note="12 repeat: matches 2638..2747 of consensus"
repeat_region	23173..23288	/note="MIR repeat: matches 13..126 of consensus"
repeat_region	23472..23858	/note="MER70A repeat: matches 127..545 of consensus"
misc_feature	26500..26778	/note="match: GSS A0192529"
repeat_region	26856..27160	/note="Alusq repeat: matches 1..301 of consensus"
repeat_region	27460..27770	/note="Alusq repeat: matches 1..311 of consensus"
repeat_region	27999..28292	/note="Alub repeat: matches 1..305 of consensus"
repeat_region	29036..29175	/note="2 copies 70 mer 84% conserved"
repeat_region	29037..29168	/note="2 copies 66 mer 83% conserved"
repeat_region	29040..29119	/note="5 copies 16 mer 73% conserved"
repeat_region	29048..29167	/note="5 copies 24 mer 70% conserved"
repeat_region	29057..29147	/note="7 copies 13 mer 69% conserved"
repeat_region	29072..29151	/note="20 copies 4 meraat 66% conserved"
repeat_region	29200..29504	/note="Alusq repeat: matches 1..304 of consensus"
repeat_region	29581..29692	/note="7 copies 16 mer 69% conserved"
repeat_region	29690..29725	/note="18 copies 2 mer ta 81% conserved"
repeat_region	29766..29865	/note="DIPAS repeat: matches 5943..6042 of consensus"
repeat_region	29872..29911	/note="20 copies 2 mer aa 80% conserved"
repeat_region	30042..30253	/note="1mer3 repeat: matches 5337..6164 of consensus"
repeat_region	30493..30540	/note="3 copies 16 mer 88% conserved"
Query Match	36.3%: Score 43.6; DB 9; Length 131427;	
Best Local Similarity	65.3%: Pred.No.0.0091;	
Matches	64; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
QY	22	agaagagcaggaccttgggagcaagaatatctaagttaattcctgaactcgtatatta 81
Db	81097	AGGTGGGCGATGGATTGGGACCCAGAAAGCCACGATTCAATCTGCATCGACACTTA 81038
QY	82	ttaactaacatctcttggccaatggtcttaagctttt 119
Db	81037	CTAGCTATGTGGCTTTGGGCAATTAATTAACAACCTCTCT 81000
RESULT	15	
LOCUS	AC064798	157185 bp DNA Linear HTG 17-MAY-2000
DEFINITION	AC064798	Homo sapiens chromosome 1 clone RP11-182C20 map 1, WORKING DRAFT
ACCESSION	AC064798	GI:7885063
VERSION	AC064798.2	GI:7885063

RESULT	15
LOCUS	AC064798
DEFINITION	AC064798 157185 bp DNA linear HTG 17-MAY-2000
ACCESSION	HOMO sapiens chromosome 1 clone RP11-182C20 map 1, WORKING DRAFT
VERSION	AC064798.2 GI:7885063

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 14:51:24 : Search time 8462.63 Seconds
(without alignments)
31.898 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactacctaagagatcatct 20

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	256	9 A1629829	A1629829 486039F12
2	18.4	92.0	527	10 BG267668	BG267668 1000135F1
3	17.4	87.0	632	9 AW943206	AW943206 LD33880.3
4	17.4	87.0	714	12 AZ966012	AZ966012 2M0236018
5	17.4	87.0	1028	12 CNS010LK	AL099122 Drosophila
6	17.4	87.0	1101	12 CNS0024V	AL062157 Drosophila
7	16.8	84.0	320	9 BB066589	BB066589 BB066589
8	16.8	84.0	331	9 BB559660	BB559660 BB559660
9	16.8	84.0	374	12 A2110509	A2110509 RPCI-23-4
10	16.8	84.0	409	12 A0475625	A0475625 CIRBI-E1
11	16.8	84.0	424	12 BH400996	BH400996 AG-ND-124
12	16.8	84.0	442	9 AL509860	AL509860 AL509860
13	16.8	84.0	540	12 BB8004	BB8004 RPCI1-16C2
14	16.8	84.0	576	12 AZ483186	AZ483186 1M0308N08
15	16.8	84.0	673	9 AV834315	AV834315 AV834315
16	16.8	84.0	785	12 BH116550	BH116550 RPCI-24-2
17	16.8	84.0	831	10 BE704507	BE704507 SC01_05H0

C 18	16.4	82.0	269	9 AV016820	AV016820 AV016820
19	16.4	82.0	407	12 A0814525	A0814525 HS_5265_A
20	16.4	82.0	812	12 BH268838	BH268838 CH230-162
21	16	80.0	849	10 BG445507	BG445507 GA_Ea002
22	15.8	79.0	208	12 A2509241	A2509241 1M0352P04
23	15.8	79.0	287	10 Z28847	Z28847 HSBAS5E061 S
24	15.8	79.0	328	9 AU097685	AU097685 AU097685
25	15.8	79.0	330	10 BF331881	BF331881 OVI-BT063
26	15.8	79.0	341	9 AV645999	AV645999 AV645999
27	15.8	79.0	343	12 BH041588	BH041588 RPCI-24-3
28	15.8	79.0	368	10 T87445	T87445 yd69h05.r1
29	15.8	79.0	378	12 B27343	B27343 TSD14TR TAM
30	15.8	79.0	385	9 AM802137	AM802137 I15-UM007
31	15.8	79.0	403	12 A0147024	A0147024 HS_2269-A
32	15.8	79.0	416	9 BE120640	BE120640 UI-R-CA0-
33	15.8	79.0	418	12 A2445420	A2445420 1M0241M12
34	15.8	79.0	433	12 A0716681	A0716681 HS_5463_A
35	15.8	79.0	442	10 N41676	N41676 yw90e07.r1
36	15.8	79.0	446	12 A0436731	A0436731 HS_5068_B
37	15.8	79.0	459	10 BF413605	BF413605 UI-R-CA0-
38	15.8	79.0	459	10 BF413606	BF413606 UI-R-CA0-
39	15.8	79.0	469	12 B65834	B65834 CIT-HSP-202
40	15.8	79.0	486	12 A2695007	A2695007 UP_312-24
41	15.8	79.0	493	12 A0205575	A0205575 HS_3225_A
42	15.8	79.0	493	12 A0304517	A0304517 HS_3138_B
43	15.8	79.0	495	10 N29129	N29129 yx47e08.r1
44	15.8	79.0	497	12 A0880539	A0880539 HS_5045_B
45	15.8	79.0	499	9 AA401233	AA401233 zv63e02.r

ALIGNMENTS

RESULT 1
A1629829
LOCUS 486039F12.x3 486 - leaf primordia cDNA library from Hake lab Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION A1629829
VERSION A1629829.1 GI:4681159
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 256)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 486039 row: F column: 12.
LOCATION/Qualifiers
FEATURES
source 1..256
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="486 - leaf primordia cDNA library from Hake lab"
/tissue_type="leaf primordia"
/dev_stage="P7-p11 leaf"
/lab_host="E.coli XL1-blue MFR"
/note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA library."
BASE COUNT 69 a 70 c 51 g 66 t
ORIGIN

Query Match	92.0%;	Score 18.4;	DB 9;	Length 256;
Best Local Similarity	95.08;	Pred. No. 87;		
Matches 19; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	aaactacctaagacatct	20
Db	178	AAACTACTGAGAGCTACT	197

RESULT 2
BG267668

LOCUS	527 bp	linear	EST 20-FEB-2001
DEFINITION	Unigene I from Maize Genome Project Zea mays		
CDNA	mRNA sequence.		
ACCESSION	U06575		

ACCESSION	BG267668
VERSION	BG267668.1
KEYWORDS	EST.
SOURCE	Zea mays.
ORGANISM	Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 527)

TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL	Unpublished (1999)
COMMENT	Contact: Walbot V

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel.: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1000135 row: F column: 11.

```

FEATURES      location/Qualifiers
source        1. .527

```

```

/organism="Zea mays"
/db_xref="dbEST:486039f12.x3"
/db_xref="taxon:4577"
/clone_idb="1000 - Unigene I from Maize Genome Project"
/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660, 6633
, 687, 707, and 945. Contigs were assembled using TIGR's
CAP program and a representative EST from each contig was
selected for the unigene set. All singlets were also
selected."

```

BASE COUNT	151 a	121 c	119 g	136 t
ORIGIN				

Query Match	92.0%	Score 18.4	DB 10	Length 527
Best Local Similarity	95.0%	Pred. No. 1e+02		
Matches 19, Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	db	1	20
aaactaacctaagagctatct	203	1	222

RESULT	3			
AM943206/c				
LOCUS	AM943206	622 bp	mRNA	linear
DEFINITION	LD33880.3	prime	LD Drosophila melanogaster embryo port2	EST 23-APR-2001

ACCESSION
VERSION
AM943206.1
GI:8120917
melanogaster cDNA clone LD33880.3 similar to AC005711: Drosophila melanogaster, chromosome 2L, region 33D3-33E8, BAC clone BACR48M09, complete sequence, mRNA sequence.
AM943206
AM943206.1

KEYWORDS • EST.
SOURCE fruit fly.

ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 622)

REFERENCE

AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,

TITLE Lewis, S. and Rubin, S.M.
JOURNAL BDGP/HHMI Drosophila EST Project
COMMENT Unpublished (2001)
Other_ESTs: LD33860..5prime

Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd,
Berkeley, CA 94720, USA
Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST/esterfruitfly.pearkeley.edu>
Based upon the presence of a xhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. h11 genomic AE003636: Drosophila melanogaster genomic scaffold 14200001386055 section 29 of 63, complete sequence: 03/12/2001 Plate: LD 338 row: G column: 8
High quality sequence stop:443.

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FEATURES      Location/Qualifiers
source        1. .622
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BASE COUNT	128 a	153 c	167 g	173 t	1 others
/organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="LD33880" /clone_1lp="LD Drosophila melanogaster embryo pot2" /sex="male and female" /dev_stage="0 to 24 hours mixed stage embryonic" /lab_host="XLI Blue" /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2 XhoI; Sized fractionated cDNAs were directly ligated into pOT2."					

Query Match	87.0%	Score 17.4;	DB 9;	Length 622;
Best Local Similarity	94.7%;	Pred. No. 3.2e+02;		
Matches 18;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 1 aaactactaagatc 19
||||||| |||||
Db 211 AAACCTACCCAGAGCTATC 193

LOCUS	DEFINITION	RESULT 4
AZ966012	Mouse 10kb plasmid pUCG2M library Mus musculus genomic	714 bp DNA linear GSS 27-APR-2001

clone UUGC2M0236018 F, DNA sequence.
A2966012

```

VERSION      A2966012.1  GI:13837239
KEYWORDS     GSS.
SOURCE       house mouse.

```

ORGANISM
Mus musculus
Edkaryota: Metazoa: Chordata: Cranialta: Euteleostomi:
Mammalia: Eutheria: Rodentia: Scturognathi: Muridae: Mus.
1 (bases 1 to 714)
Dunn, D.G., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
REFERENCE
AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

Journal Comment
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: 0 column: 18
Seq primer: CATTGTAAACGACGCGCTAGT
Class: plasmid ends
High quality sequence stop: 714.
Location/Qualifiers

FEATURES

source

1. 714
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0236018"
/clone.lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

258 a 151 c 163 g 142 t

Query Match 87.0%; Score 17.4; DB 12; Length 714;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 aactacctaagactatct 20
|||||
DB 76 AACCACTAAGACTATCT 94

RESULT 5
CNS010LK/c 1028 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence sp6 end of BAC
DEFINITION BACN04103 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL099122 GI:5610733
VERSION AL099122.1
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1028)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -

http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES

source

Location/Qualifiers
1. 1028
/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone.lib="DrosBAC"
/clone="BACN04103"
/note="end : sp6"

BASE COUNT 231 a 244 c 250 g 285 t 18 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 12; Length 1028;
Best Local Similarity 94.7%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 aactacctaagactatct 19
|||||
DB 461 AACCTACCAAGACTATC 443

RESULT 6
CNS0024V 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR05E09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL062157 GI:4940317
VERSION AL062157.1
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

Location/Qualifiers
1. 1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone.lib="RPCI-98"
/clone="BACR05E09"
/note="end : T7"

BASE COUNT 297 a 255 c 248 g 250 t 51 others
ORIGIN

QY	1	aactactaagaagcattc 19	87.0%	Score 17.4	DB 12	Length 1101
Db	628	AAACTACCCAGAGCTATC 646	Best Local Similarity 94.7%	Pred. No. 3,6e+02		
Matches	18	Conservative	0	Mismatches	1	Indels
					0	Gaps
					0	

RESULT	7	
BB066589	320 bp	MRNA linear
LOCUS		EST 25-JUN-2000
DEFINITION	BB066589 RIKEN full-length enriched, 15 days embryo male testis Mus musculus cDNA clone 8030453F10 3 similar to U49385 Mus musculus	
ACCESSION	BB066589	
VERSION	BB066589.1	GI:8524003
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 320)	
AUTHORS	Kono,H., Alizawa,K., Akahira,S., Akiyama,J., Arai,Kawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hata,A., Hayatsu,N., Hirozane,T., Hoti,F., Ishii,T., Ishikawa,U., Ishikawa,T., Itoh,M., Itawa,M., Kadota,K., Kagawa,T., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,Y., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomioka,N., Toya,T., Tsunoda,Y., Watanishi,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	
TITLE	RIKEN Mouse ESTs (Kono/H., et al.)	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gs.c.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotranscription and thermoinactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (3), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.	

FEATURES	source
Location/Qualifiers	
1..320	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="8030453F10"	
/clone_lib="RIKEN full-length enriched, 15 days embryo male testis"	
/sex="male"	
/tissue_type="testis"	
/dev_stage="15 days embryo"	
/lab_host="DH10B"	

/note="Site.1: Sali; site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGGAGAGAGATCCAGACACTCTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 185.0 Second strand cDNA was prepared with the primer adapter of sequence [5', GAGGAGAGATCTTCGAGTTAAATTAAATTATATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified p Bluescript KS(+) after bulk excision from LambdaFLC I. Cloning sites, 5' end: Sali; 3' end: BamHI"


```

/db_xref="taxon:9606"
/clone="2589J3"
/clone_11b="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT      122 a      54 c      64 g      168 t      1 others
ORIGIN

Query Match      84.0%; Score 16.8; DB 12; Length 409;
Best Local Similarity 90.0%; Pred. No. 5.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 aaactactaagagctatct 20
        |||||
Db      215 AAACCTACCTAAGATCATCT 196

RESULT 11
BHA00996
LOCUS      BHA00996      424 bp      DNA      linear      GSS 11-DEC-2001
DEFINITION AG-ND-12404.TF ND-TAM Anopheles gambiae genomic clone AG-ND-12404,
            DNA sequence.
ACCESSION   BHA00996
VERSION     BHA00996.1 GI:17347212
KEYWORDS    GSS.
SOURCE      African malaria mosquito.
ORGANISM    Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae
            ; Anopheles.
REFERENCE   1 (bases 1 to 424)
AUTHORS    Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE      Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL     Unpublished (2001)
COMMENT     Other_GSSs: AG-ND-12404.TR
            Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjoftus@tigr.org
            This clone is from an A. gambiae BAC library (ND-TAM) provided by
            F.H. Collins and sequenced by The Institute for Genomic Research
            (TIGR). The BAC library was generated from A. gambiae PEST strain
            DNA. All DNA was extracted from newly hatched first instar larvae
            to minimize the inclusion of DNA from microorganisms that inhabit
            the gut. The DNA is derived from mixed sexes of larvae. The BAC
            library was constructed at Texas A&M University BAC Center
            University, College Station, Texas 77843-2123, USA using a HindIII
            partial digest.
            Seg primer: M13 For
            Class: BAC ends
            Location/Qualifiers
                location=1..424
                /organism="Anopheles gambiae"
                /strain="PEST"
                /db_xref="taxon:7165"
                /clone="AG-ND-12404"
                /clone_11b="ND-TAM"
                /note="Vector: pECBAC1; Site_1: HindIII"
BASE COUNT      159 a      93 c      65 g      107 t
ORIGIN

Query Match      84.0%; Score 16.8; DB 12; Length 424;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 aaactactaagagctatct 20

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||| ||| ||||| ||||| |||||
Db      140 AAAATACATAGAGCTATCT 159

RESULT 12
AL509860
LOCUS      AL509860      442 bp      mRNA      linear      EST 04-JAN-2001
DEFINITION Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
            Hordeum vulgare cDNA clone HY03B17u 3', mRNA sequence.
ACCESSION   AL509860
VERSION     AL509860.1 GI:12036363
KEYWORDS    EST.
SOURCE      Hordeum vulgare
            barley.
            Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
            ; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 442)
AUTHORS    Michalek,M., Weschke,W., Pleissner,K.-P. and Graner,A.
TITLE      EST sequencing and analysis in barley
JOURNAL     Unpublished (2000)
COMMENT     Contact: Michael M
            Institute for Plant Genetics and Crop Plant Research
            Corrensstr.3, D-06466 Gatersleben, Germany
            Email: michael@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
            Seq primer: M13uni primer for 3' end.
            Location/Qualifiers
                location=1..442
                /organism="Hordeum vulgare"
                /cultivar="Barke"
                /db_xref="taxon:4513"
                /clone="HY03B17u"
                /clone_11b="Hordeum vulgare Barke developing caryopsis
                (3.-15.DAP)"
                /tissue_type="developing caryopsis (3.-15.DAP)"
                /lab_host="XLDLR"
                /note="Vector: Plasmid pBK-CMV; Site_1: EcoRI; Site_2:
                XhoI; mRNA was made from developing caryopsis (3.-15.DAP)
                of spring barley variety 'Barke', a high quality malting
                variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
                (3'-end of cDNA). NOTE: Due to a cloning artefact caused
                by the kit, in most cases the EcoRI site is NOT present,
                as well as the EcoRI adapter. Average insert size is 1 kb
                Sequence trimming: Vector sequences and sequence ends were
                trimmed from the 5'- and 3'-end until a 50 bp window
                contained less than two ambiguities. The maximum length was
                set to 700 bp"
BASE COUNT      115 a      117 c      84 g      124 t      2 others
ORIGIN

Query Match      84.0%; Score 16.8; DB 9; Length 442;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 aaactactaagagctatct 20
        |||||
Db      333 AGACTACCTCAGAGCTATCT 352

RESULT 13
B88004/c
LOCUS      B88004      540 bp      DNA      linear      GSS 09-APR-1999
DEFINITION RPI11-16C24.FPB RPI1-11 Homo sapiens genomic clone RPI1-11-16C24,
            DNA sequence.
ACCESSION   B88004
VERSION     B88004.1 GI:2929136
KEYWORDS    GSS.
SOURCE      human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 540)

```

AUTHORS

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P., and Venter, J.C.

TITLE

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

JOURNAL

Unpublished (1998)

COMMENT

Other GSSs: RPC11-16C24.TP RPC11-16C24.TVB
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208

Email: mdamas@tigr.org
Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@tigr.org), please contact Pieter de Jong (pieter@tigr.org), please contact Pieter de Jong (pieter@tigr.org) or from BACAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="GDB:7505831"
/db_xref="taxon:9606"
/clone="RPC1-11-16C24"
/clone.lib="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"

BASE COUNT 187 a 104 c 106 g 143 t
ORIGIN

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 12; Length 540;
Matches 18; Conservativity 0; Pred. No. 5.9e+02; Indels 0; Gaps 0;

1 aaactacctaagagctatct 20

186 AACCTACTTAGAGCTATAT 167

RESULT 14

AZ483186/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

576 bp DNA linear GSS 05-OCT-2000
1M0308N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0308N08 R, DNA sequence.
AZ483186
AZ483186
GI:10646948
GSS.
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 576)
Dunn, D., Aoyagi, A., Barber, M., Beaumont, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, R., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Seq plate: 0308 row: N column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 576.

FEATURES

source

1..576
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0308N08"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-gold, TI-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (911473211419b/AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 166 a 91 c 113 g 206 t
ORIGIN

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 12; Length 576;
Matches 18; Conservativity 0; Pred. No. 6e+02; Indels 0; Gaps 0;

1 aaactacctaagagctatct 20

489 AAGATACCTTAGAGCTATCT 470

RESULT 15

AV834315

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

673 bp mRNA linear EST 22-JUN-2001
AV834315 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
clone rbags14a02, mRNA sequence.
AV834315
AV834315
GI:14526404
EST.
Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 673)
Sato, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2001)
Contact: Kazuhito Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL: http://www.rib.okayama-u.ac.jp/barley/
sato,k., Saitoh, D., Takeda, K., Shini, T., and Kohara, Y. Direct
submission:
database: http://www.shigen.nig.ac.jp/barley/Barley.html.

FEATURES

source

Location/Qualifiers
1 673

1. .673

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/organism="Hordeum vulgare subsp. vulgare"  
/cultivar="Haruna Nijo"
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/calci_val= Hal und NJO
/db_xref="taxon:112509"
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/db_xref="taxon:112509"
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/clone="rbags14a02"
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/clone_lib="K. Sato unpublished cDNA library: Hordeum  
vulgare subsp. vulgare shoots germination"
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vulgaris subsp. vulgaris shoots germination"

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/tissue_type="shoots"

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/dev_stage="germination"
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a	172	c	133	g	165	t
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BASE COUNT
ORIGIN

203 a	172 c	133 g	165 t
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Query Match
Best Total

84.08; Score 16.8; DB 9; Length 673;
90.08; Pred NO. 6 2e+02;

Best Local Similarity 90.0%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 3

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

Db 500 AGACTACCTCAGAGCTATCT 519

Search completed: September 7, 2002, 14:51:28
Job time: 16187 sec

Job time: 161.87 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2002, 01:09:44 ; Search time 1826.34 Seconds
(without alignments)
33.350 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactacctaagagctatct 20

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2036664 seqs, 1522705736 residues
Total number of hits satisfying chosen parameters: 4073328

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New:
1: /cgn2_6/prodata/2/pna/PCN_NEW_COMB.seq:*
2: /cgn2_6/prodata/2/pna/US06_NEW_COMB.seq:*
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4: /cgn2_6/prodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/prodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/prodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	45121	6	US-10-035-832-1262 Sequence 1262, Ap
2	17.4	87.0	96599	6	US-10-035-832-1349 Sequence 1349, Ap
3	16.8	84.0	461	6	US-10-098-754-5310 Sequence 5310, Ap
4	16.8	84.0	1022	7	US-10-027-632-258416 Sequence 258416, Ap
5	16.8	84.0	1022	7	US-10-027-632-258417 Sequence 258417, Ap
6	16.8	84.0	1223	6	US-10-098-754-11812 Sequence 11812, A
7	16.8	84.0	2500	7	US-10-027-632-111702 Sequence 111702, A
8	16.8	84.0	2500	7	US-10-027-632-111703 Sequence 111703, A
9	15.8	79.0	337	5	US-09-721-844-17137 Sequence 17137, A
10	15.8	79.0	498	7	US-10-027-632-50682 Sequence 50682, A
11	15.8	79.0	498	7	US-10-027-632-50683 Sequence 50683, A
12	15.8	79.0	498	7	US-10-027-632-50684 Sequence 50684, A
13	15.8	79.0	498	7	US-10-027-632-50685 Sequence 50685, A
14	15.8	79.0	1022	1	PCT-US02-12378-67 Sequence 67, Appl
15	15.8	79.0	1022	7	US-10-124-805-67 Sequence 67, Appl
16	15.8	79.0	1592	5	US-09-705-256A-1146 Sequence 1146, Ap
17	15.8	79.0	2774	7	US-10-104-047-248 Sequence 248, App
18	15.8	79.0	5775	6	US-10-198-846-9873 Sequence 9873, Ap
19	15.4	77.0	129710	7	US-10-027-632-178902 Sequence 178902, A
20	15.2	76.0	118	5	US-09-698-495-511 Sequence 511, App
21	15.2	76.0	401	5	US-10-027-632-185243 Sequence 185243, A
22	15.2	76.0	455	7	US-10-027-632-185243 Sequence 185243, A
23	15.2	76.0	498	6	US-10-182-995-2106 Sequence 2106, Ap
24	15.2	76.0	498	6	US-10-203-136-2167 Sequence 2167, Ap
25	15.2	76.0	498	6	US-10-182-993-2148 Sequence 2148, Ap

ALIGNMENTS

c 26	15.2	76.0	498	6	US-10-182-997-2121	Sequence 2121, Ap
c 27	15.2	76.0	498	6	US-10-182-998-2092	Sequence 2092, Ap
c 28	15.2	76.0	498	6	US-10-203-135-2064	Sequence 2064, Ap
c 29	15.2	76.0	498	6	US-10-203-137-2220	Sequence 2220, Ap
c 30	15.2	76.0	498	6	US-10-203-139-2197	Sequence 2197, Ap
c 31	15.2	76.0	571	7	US-10-027-632-201021	Sequence 201021, A
c 32	15.2	76.0	582	7	US-10-027-632-274673	Sequence 274673, A
c 33	15.2	76.0	637	7	US-10-027-632-226676	Sequence 226676, A
c 34	15.2	76.0	915	7	US-10-156-995-16	Sequence 16, Appl
c 35	15.2	76.0	915	7	US-10-156-995-71	Sequence 71, Appl
c 36	15.2	76.0	946	7	US-10-027-632-120073	Sequence 120073, A
c 37	15.2	76.0	1045	7	US-10-027-632-119014	Sequence 119014, A
c 38	15.2	76.0	1143	7	US-10-027-632-201020	Sequence 201020, A
c 39	15.2	76.0	1143	8	US-60-360-039-46954	Sequence 46954, A
c 40	15.2	76.0	12304	6	US-10-205-428-677	Sequence 677, App
c 41	15	75.0	30042	6	US-10-080-170-650	Sequence 650, App
c 42	15	75.0	30042	7	US-10-080-170B-650	Sequence 650, App
c 43	14.8	74.0	235	5	US-09-539-331D-2086	Sequence 2086, Ap
c 44	14.8	74.0	378	5	US-09-918-995-37657	Sequence 37657, A
c 45	14.8	74.0	523	7	US-10-027-632-93635	Sequence 93635, A

RESULT 1
US-10-035-832-1262
; Sequence 1262, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Engelhard, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1262
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-035-832-1262

Query Match 100.0%; Score 20; DB 6; Length 45121;
Best Local Similarity 100.0%; Pred. No. 0.89; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 aaactacctaagagctatct 20
Db 9260 aaactacctaagagctatct 9279

RESULT 2
US-10-035-832-1349
; Sequence 1349, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Engelhard, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1

```

; SEQ ID NO 1349
; LENGTH: 96599
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3729)..(3748)
; OTHER INFORMATION: "n" at positions 3729 thru 3748 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4902)..(4921)
; OTHER INFORMATION: "n" at positions 4902 thru 4921 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7901)..(8020)
; OTHER INFORMATION: "n" at positions 7901 thru 8020 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12187)..(12206)
; OTHER INFORMATION: "n" at positions 12187 thru 12206 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36676)..(36765)
; OTHER INFORMATION: "n" at positions 36676 thru 36765 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51928)..(51947)
; OTHER INFORMATION: "n" at positions 51928 thru 51947 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56214)..(56713)
; OTHER INFORMATION: "n" at positions 56214 thru 56713 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (58367)..(58386)
; OTHER INFORMATION: "n" at positions 58367 thru 58386 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (63327)..(63350)
; OTHER INFORMATION: "n" at positions 63327 thru 63350 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (66416)..(66549)
; OTHER INFORMATION: "n" at positions 66416 thru 66549 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (67304)..(67872)
; OTHER INFORMATION: "n" at positions 67304 thru 67872 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (84883)..(84902)
; OTHER INFORMATION: "n" at positions 84883 thru 84902 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (91740)..(91802)
; OTHER INFORMATION: "n" at positions 91740 thru 91802 can be any base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (95348)..(95367)
; OTHER INFORMATION: "n" at positions 95348 thru 95367 can be any base
US-10-035-832-1349

Query Match      87.0%; Score 17.4; DB 6; Length 96599;
Best Local Similarity 94.7%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 aaactactaagagctatc 19
|||||
Db 22555 aaactactaagagctatc 22573
```

RESULT 3

```

US-10-098-754-5310
; Sequence 5310, Application US/10098754
; GENERAL INFORMATION:
; APPLICANT: Harrington, John J.
; APPLICANT: Jackson, P. David
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Cain, Scott
; APPLICANT: Rundlett, Stephen E.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
; FILE REFERENCE: AIX-001CN
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/791539
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 21107
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5310
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-754-5310

Query Match      84.0%; Score 16.8; DB 6; Length 461;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 aaactactaagagctatc 20
|||||
Db 283 aaactactaagagctatc 302
```

```

RESULT 4
US-10-027-632-258416
; Sequence 258416, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258416
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-258416
```

```

Query Match      84.0%; Score 16.8; DB 7; Length 1022;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 aaactactaagagctatc 20
|||||
Db 902 aaactactaagagctatc 921
```

RESULT 5
US-10-027-632-258417
; Sequence 258417, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 258417
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-258417

Query Match 84.0%; Score 16.8; DB 7; Length 1022;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
||||| ||||||| |||||

DB 902 aaactacctaagatcatct 921

RESULT 6
US-10-098-754-11812
; Sequence 11812, Application US/10098754
; GENERAL INFORMATION:
; APPLICANT: Harrington, John J.
; APPLICANT: Jackson, P. David
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Cain, Scott
; APPLICANT: Rundlett, Stephen E.
; APPLICANT: Ramachandran, Rakesh
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND PROTEIN HOMOLOGS AND USES THEREOF
; FILE REFERENCE: AIX-001CN
; CURRENT APPLICATION NUMBER: US/10/098,754
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 09/791539
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 21107
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 11812
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1223)
; OTHER INFORMATION: n = A,T,C or G
US-10-098-754-11812

Query Match 84.0%; Score 16.8; DB 6; Length 1223;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
||||| ||||||| |||||

DB 347 aaactgctaagagcatct 366

RESULT 7
US-10-027-632-111702
; Sequence 111702, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 111702
; LENGTH: 2500
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-111702

Query Match 84.0%; Score 16.8; DB 7; Length 2500;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
||||| ||||||| |||||

DB 1358 aaactgctaagagcatct 1377

RESULT 8
US-10-027-632-111703
; Sequence 111703, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

```
;; PRIOR APPLICATION NUMBER: US 60/146,002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 111703
;; LENGTH: 2500
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-111703
```

```
Query Match      84.0%; Score 16.8; DB 7; Length 2500;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 1 aactacctaagactatct 20
Db 1358 aactcctaagaagcattct 1377
```

```
RESULT 9
US-09-721-544-17137/C
; Sequence 17137, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Slimin
; APPLICANT: Dickinson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogueira, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fel
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 2489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17137
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-17137
```

```
Query Match      79.0%; Score 15.8; DB 5; Length 337;
Best Local Similarity 89.5%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 2 aactacctaagactatct 20
Db 133 ACCTACTAATAGCTATCT 115
```

```
RESULT 10
US-10-027-632-50682
; Sequence 50682, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50682
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50682
```

```
Query Match      79.0%; Score 15.8; DB 7; Length 498;
Best Local Similarity 89.5%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 2 aactacctaagactatct 20
Db 473 agtactacctaagacttct 491
```

```
RESULT 11
US-10-027-632-50683
; Sequence 50683, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
```


; SEQ ID NO 50683
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50683

Query Match
Best Local Similarity 89.0%; Score 15.8; DB 7; Length 498;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aactacctaagagctatct 20
| ||||| ||||| |||
DB 473 agctacctaagagcttctt 491

RESULT 12
US-10-027-632-50684
; Sequence 50684, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50684
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50684

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 7; Length 498;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aactacctaagagctatct 20
| ||||| ||||| |||
DB 473 agctacctaagagcttctt 491

RESULT 13
US-10-027-632-50685
; Sequence 50685, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50685
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50685

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 7; Length 498;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aactacctaagagctatct 20
| ||||| ||||| |||
DB 473 agctacctaagagcttctt 491

RESULT 14
PCT-US02-12378-67
; Sequence 67, Application PC/TUS0212378
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margareta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.47003PC
; CURRENT APPLICATION NUMBER: PCT/US02/12378
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-12378-67

Query Match
Best Local Similarity 89.5%; Score 15.8; DB 1; Length 1022;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aactacctaagagctatct 20
| ||||| ||||| |||
DB 539 accctacctaagagctatct 557

RESULT 15
US-10-124-805-67
; Sequence 67, Application US/10124805
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.

```

:
: APPLICANT: Sleath, Paul R.
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
:
: TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
:
: FILE REFERENCE: 210121.470c12
:
: CURRENT APPLICATION NUMBER: US/10/124,805
:
: CURRENT FILING DATE: 2002-04-15
:
: NUMBER OF SEQ ID NOS: 627
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 67
:
: LENGTH: 1022
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-10-124-805-67

```

Query Match	79.0%	Score 15.8	DB 7	Length 1022
Best Local Similarity	89.5%	Pred. NO.1e+02		
Matches 17	Conservative	0	Mismatches 2	Indels 0
Gaps				
OY	2	aactaactaagactatct	20	
db	539	aactaactaactagcatct	557	

Search completed: September 8, 2002, 01:09:47
Job time: 37065 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:31:46 : Search time 13836.9 seconds
(without alignments)
31.271 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactacctaagactatct 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/2/pna/PCRTUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
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11: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
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13: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
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19: /cgn2_6/ptodata/2/pna/US096_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US097_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US098_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US099_COMB.seq:*
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42: /cgn2_6/ptodata/2/pna/US119_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US120_COMB.seq:*

Result	No.	Score	Query	Length	ID	Description
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2	20	100.0	40	32	US-09-834-291-22	Sequence 22, Appl
3	20	100.0	40	32	US-09-834-291-30	Sequence 30, Appl
4	20	100.0	1608	7	US-08-377-522-1	Sequence 1, Appl1
5	20	100.0	1608	7	US-08-377-522-1	Sequence 1, Appl1
6	20	100.0	1608	7	US-08-377-522-1	Sequence 1, Appl1
7	20	100.0	2165	26	US-09-665-615B-94	Sequence 94, Appl
8	20	100.0	2165	31	US-09-802-669-94	Sequence 94, Appl
9	20	100.0	2280	32	US-09-834-291-3	Sequence 3, Appl1
10	20	100.0	2827	32	US-09-834-291-4	Sequence 4, Appl1
11	20	100.0	3212	32	US-09-834-291-1	Sequence 1, Appl1
12	20	100.0	45121	36	US-09-997-722-10	Sequence 10, Appl1
13	18.4	92.0	238	17	US-09-298-328A-1327	Sequence 1327, Ap
14	18.4	92.0	238	47	US-50-085-147-1327	Sequence 8707, Ap
15	18.4	92.0	285	17	US-09-303-031A-8707	Sequence 8707, Ap
16	18.4	92.0	285	33	US-09-894-949-8707	Sequence 8707, Ap
17	18.4	92.0	290	17	US-09-894-949A-8707	Sequence 8707, Ap
18	18.4	92.0	290	17	US-09-303-031A-7338	Sequence 7338, Ap
19	18.4	92.0	290	33	US-09-894-949A-7338	Sequence 7338, Ap
20	18.4	92.0	290	33	US-09-894-949A-7338	Sequence 7338, Ap
21	18.4	92.0	370	33	US-09-865-439A-11835	Sequence 11835, A
22	18.4	92.0	458	17	US-09-306-350A-14682	Sequence 14682, A
23	18.4	92.0	458	34	US-09-909-629-14682	Sequence 80806, A
24	18.4	92.0	487	33	US-09-873-402A-80806	Sequence 80806, A
25	18.4	92.0	487	59	US-60-209-830-52545	Sequence 52545, A
26	18.4	92.0	527	33	US-09-873-402A-3718	Sequence 3718, Ap
27	18.4	92.0	527	59	US-60-209-830-3718	Sequence 3718, Ap
28	18.4	92.0	637	33	US-09-873-402A-3631	Sequence 3631, Ap
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31	18.4	92.0	639	59	US-60-207-458-115280	Sequence 115280,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 36 18.4 92.0 1529 28 US-09-708-427-73361 Sequence 73361, A
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C 42 17.4 87.0 2815 23 US-09-614-150-11371 Sequence 11371, A
C 43 17.4 87.0 2815 23 US-60-191-637-11403 Sequence 11403, A
C 44 17.4 87.0 3679 55 US-60-167-217-11396 Sequence 11396, A
C 45 17.4 87.0 3916 23 US-09-614-150-13759 Sequence 13759, A
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ALIGNMENTS

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RESULT 1
US-09-834-291-16
; Sequence 16, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-16
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Query Match 100.0%; Score 20; DB 32; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 1 aaactacctaagagctatct 20
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RESULT 2
US-09-834-291-22
; Sequence 22, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo Sapiens
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US-09-834-291-22

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Query Match 100.0%; Score 20; DB 32; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 aaactacctaagagctatct 20
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Db 11 aaactacctaagagctatct 30
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RESULT 3
US-09-834-291-30
; Sequence 30, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-30
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Query Match 100.0%; Score 20; DB 32; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 aaactacctaagagctatct 20
    |||
Db 11 aaactacctaagagctatct 30
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RESULT 4
US-08-377-522-1
; Sequence 1, Application US/08377522
; GENERAL INFORMATION:
; APPLICANT: Mountz, John D.
; APPLICANT: Liu, Changdan
; APPLICANT: Cheng, Jianhua
; APPLICANT: Koopman, William J.
; APPLICANT: Zhou, Tong
; TITLE OF INVENTION: Human Fas Gene Promoter Region
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,522
; FILING DATE: 20-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

NAME: Sertlich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UOAB:034/SER
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1467..1496
US-08-377-522-1

Query Match 100.0%; Score 20; DB 7; Length 1608;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactactaagaagctatct 20
|||||
Db 507 AACCTACTAGAGCTATCT 526

RESULT 5
US-08-377-522C-1
Sequence 1, Application US/08377522C
GENERAL INFORMATION:
APPLICANT: Mountz et al.
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: TX
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522C
FILING DATE: January 20, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 bp
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:

ORGANISM: human
TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIX1; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
US-08-377-522C-1

Query Match 100.0%; Score 20; DB 7; Length 1608;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactactaagaagctatct 20
|||||
Db 507 AACCTACTAGAGCTATCT 526

RESULT 6
US-08-377-522D-1
Sequence 1, Application US/08377522D
GENERAL INFORMATION:
APPLICANT: Mountz et al.
TITLE OF INVENTION: Human Fas Gene Promoter Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: TX
ZIP: 77071
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522D
FILING DATE: January 20, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5919
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 bp
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placental
IMMEDIATE SOURCE:
LIBRARY: (FIX1; EMBL-SP6/T7
CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:

US-08-377-522D-1

Query Match 100.0%; Score 20; DB 7; Length 1608;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||
Db 507 AAACCTAGAGCTATCT 526

RESULT 7

US-09-665-615B-94
; Sequence 94, Application US/09665615B
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-665-615B-94

Query Match 100.0%; Score 20; DB 26; Length 2165;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||
Db 821 aaactacctaagagctatct 840

RESULT 8

US-09-802-669-94
; Sequence 94, Application US/09802669
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-802-669-94

Query Match 100.0%; Score 20; DB 31; Length 2165;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||
Db 821 aaactacctaagagctatct 840

RESULT 9

US-09-834-291-3
; Sequence 3, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-3

Query Match 100.0%; Score 20; DB 32; Length 2380;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||
Db 820 aaactacctaagagctatct 839

RESULT 10

US-09-834-291-4
; Sequence 4, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-4

Query Match 100.0%; Score 20; DB 32; Length 2827;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 aaactacctaagagctatct 20
|||||

Db 1267 aaactactaagagctatct 1286

RESULT 11

US-09-834-291-1
Sequence 1, Application US/09834291

GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3212
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match 100.0%; Score 20; DB 32; Length 3212;

Best Local Similarity 100.0%; Pred. No. 8; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 aaactactaagagctatct 20

Db 1266 aaactactaagagctatct 1285

RESULT 12

US-09-997-722-10
Sequence 10, Application US/09997722

GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCE
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 45121
TYPE: DNA
ORGANISM: Homo sapiens
US-09-997-722-10

Query Match 100.0%; Score 20; DB 36; Length 45121;

Best Local Similarity 100.0%; Pred. No. 13; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 aaactactaagagctatct 20

Db 9260 aaactactaagagctatct 9279

RESULT 13

US-09-298-328A-1327/c
Sequence 1327, Application US/09298328A
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath, V.

APPLICANT: Ito, Laura, Y
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN LEAF

FILE REFERENCE: PL-0013 US
CURRENT APPLICATION NUMBER: US/09/298,328A
CURRENT FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,146
PRIOR FILING DATE: May 12, 1998
NUMBER OF SEQ ID NOS: 6550
SOFTWARE: PERL Program
SEQ ID NO 1327
LENGTH: 238

TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 700164576H1
NAME/KEY: unsure
LOCATION: 159
OTHER INFORMATION: a, t, c, g, or other
US-09-298-328A-1327

Query Match 92.0%; Score 18.4; DB 16; Length 238;

Best Local Similarity 95.0%; Pred. No. 42; Indels 1; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 aaactactaagagctatct 20

Db 209 AAACACTCTGACGACGTATCT 190

RESULT 14

US-60-085-147-1327/c
Sequence 1327, Application US/60085147

GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
NUMBER OF SEQUENCES: 6550
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/085,147
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PL-0013 P
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1327:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 700164576H1
US-60-085-147-1327

Query Match 92.0%; Score 18.4; DB 47; Length 238;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aaactacctaagactatct 20
|||||
Db 209 AAACCTACCTGAGAGCTATCT 190

RESULT 15

US-09-303-031A-8707/c
Sequence 8707, Application US/09303031A
GENERAL INFORMATION:
APPLICANT: Raghunath, Ialqudl
APPLICANT: Larosa, Thomas J.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN CALLUS
FILE REFERENCE: PL-0011 US
CURRENT APPLICATION NUMBER: US/09/303,031A
CURRENT FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/084,493
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 9627
SOFTWARE: PERL Program
SEQ ID NO 8707
LENGTH: 285
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO: 700476268H1
NAME/KEY: unsure
LOCATION: 36, 158
OTHER INFORMATION: a, t, c, g, or other
US-09-303-031A-8707

Query Match 92.0%; Score 18.4; DB 17; Length 285;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 aaactacctaagactatct 20
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Db 189 AAACCTACCTGAGAGCTATCT 170

Search completed: September 7, 2002, 22:31:48
Job time: 43802 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:21:16 ; Search time 212.3 seconds
(without alignments)
23.140 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285
Perfect score: 20
Sequence: 1 aaactactaagagatctct 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.8	84.0	6831	2 US-08-609-049A-27	Sequence 27, Appl
2	16.8	84.0	6831	4 US-09-170-996-27	Sequence 27, Appl
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4	14.2	71.0	126	1 US-07-744-282C-22	Sequence 22, Appl
5	14.2	71.0	126	1 US-07-744-282C-24	Sequence 24, Appl
6	14.2	71.0	1276	4 US-08-981-957D-12	Sequence 12, Appl
7	14.2	71.0	2809	1 US-08-484-105-3	Sequence 3, Appl
8	14.2	71.0	2809	1 US-08-484-106-3	Sequence 3, Appl
9	14.2	71.0	3119	3 US-09-299-843A-31	Sequence 31, Appl
10	14.2	71.0	3119	4 US-09-088-337B-31	Sequence 31, Appl
11	14.2	71.0	90050	4 US-09-245-041-5	Sequence 31, Appl
12	14.2	70.0	25	2 US-08-713-557B-30	Sequence 30, Appl
13	13.8	69.0	362	1 US-08-322-742-9	Sequence 9, Appl
14	13.8	69.0	631	4 US-08-998-416-670	Sequence 670, App
15	13.8	69.0	749	4 US-09-073-587-1	Sequence 1, Appl
16	13.8	69.0	2340	3 US-08-492-459-5	Sequence 5, Appl
17	13.8	69.0	2340	3 US-08-492-459-7	Sequence 5, Appl
18	13.8	69.0	2340	3 US-08-423-752-5	Sequence 7, Appl
19	13.8	69.0	2340	3 US-08-423-752-7	Sequence 5, Appl
20	13.8	69.0	2340	4 US-08-716-873-19	Sequence 19, Appl
21	13.8	69.0	2340	4 US-08-716-873-21	Sequence 19, Appl
22	13.8	69.0	2340	4 US-09-368-431-19	Sequence 19, Appl
23	13.8	69.0	2340	4 US-09-368-431-21	Sequence 21, Appl
24	13.8	69.0	2340	4 US-09-414-006-5	Sequence 5, Appl
25	13.8	69.0	2340	4 US-09-414-006-7	Sequence 7, Appl
26	13.8	69.0	3515	1 US-08-596-985-1	Sequence 1, Appl
27	13.8	69.0	4307	3 US-08-944-594-1	Sequence 1, Appl

28	13.8	69.0	4371	1 US-08-803-973-1	Sequence 1, Appl
29	13.8	69.0	4371	1 US-08-803-973-1	Sequence 1, Appl
30	13.8	69.0	176373	3 US-09-128-155-17	Sequence 17, Appl
31	13.6	68.0	48	1 US-08-374-770-2	Sequence 2, Appl
32	13.6	68.0	48	1 US-08-461-593B-2	Sequence 2, Appl
33	13.6	68.0	48	1 US-08-651-323A-2	Sequence 2, Appl
34	13.6	68.0	99	5 PCT-US92-06821A-23	Sequence 23, Appl
35	13.6	68.0	126	1 US-07-744-282C-23	Sequence 23, Appl
36	13.6	68.0	337	4 US-08-594-031-79	Sequence 79, Appl
37	13.6	68.0	683	1 US-09-328-111-168	Sequence 168, App
38	13.6	68.0	1161	1 US-08-086-439C-1	Sequence 1, Appl
39	13.6	68.0	1161	1 US-08-434-877-1	Sequence 1, Appl
40	13.6	68.0	1328	4 US-08-930-285-13	Sequence 13, Appl
41	13.6	68.0	1464	2 US-08-938-858-1	Sequence 1, Appl
42	13.6	68.0	1475	3 US-08-641-291A-92	Sequence 92, Appl
43	13.6	68.0	1531	1 US-08-449-986-1	Sequence 1, Appl
44	13.6	68.0	1531	2 US-08-756-855-1	Sequence 1, Appl
45	13.6	68.0	2447	2 US-09-014-969-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-609-049A-27
; Sequence 27, Application US/08609049A
; Patent No. 5948664
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Molz, Lisa
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609, 049A
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 148..5775
; US-08-609-049A-27

Query Match 84.0%; Score 16.8; DB 2; Length 6831;
Best Local Similarity 90.0%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
|||||
Db 6690 AAACCTACCTAAGAGCTATCT 6709

RESULT 2

US-09-170-996-27
; Sequence 27, Application US/09170996
; Patent No. 6291220
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 6291220e1 PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/170,996
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/609,049
; FILING DATE: 29-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-063700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2420
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 148..5775
; US-09-170-996-27

Query Match 84.0%; Score 16.8; DB 4; Length 6831;

Best Local Similarity 90.0%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 6690 AAACCTACCTAAGAGCTATCT 6709

RESULT 3

US-07-744-282C-21/C
; Sequence 21, Application US/07744282C
; Patent No. 5521300
; GENERAL INFORMATION:
; APPLICANT: Shah, Jyotsna S.
; APPLICANT: Nietupski, Raymond M.
; TITLE OF INVENTION: Oligonucleotides Complementary to
; TITLE OF INVENTION: Mycobacterial Nucleic Acids

NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,282C
FILING DATE: August 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrell
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: GTR90-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-07-744-282C-21

Query Match 71.0%; Score 14.2; DB 1; Length 126;

Best Local Similarity 80.0%; Pred. No. 52;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 26 AAACNACCTAAGAGCTCTTT 7

RESULT 4

US-07-744-282C-22/C
; Sequence 22, Application US/07744282C
; Patent No. 5521300
; GENERAL INFORMATION:
; APPLICANT: Shah, Jyotsna S.
; APPLICANT: Nietupski, Raymond M.
; TITLE OF INVENTION: Oligonucleotides Complementary to
; TITLE OF INVENTION: Mycobacterial Nucleic Acids
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/744,282C
; FILING DATE: August 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kevin M. Farrell
; REGISTRATION NUMBER: 35,505

1000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-713-557B-30

Query Match 70.0%; Score 14; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aaactacctaagag 14
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Db 12 AAACCTACTAAGAG 25

RESULT 13
US-08-322-742-9
Sequence 9, Application US/08322742
Patent No. 5688641
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,742
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938, 823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844, 296
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/552, 216
FILING DATE: February 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 00530/048003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 362
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-322-742-9

Query Match 69.0%; Score 13.8; DB 1; Length 362;
Best Local Similarity 88.2%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaactacctaagagcta 17
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Db 63 AAGCAACTTAAGAGCTA 79

RESULT 14
US-08-998-416-670
Sequence 670, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPYII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PE/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 670:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1446UP
US-08-998-416-670

Query Match 69.0%; Score 13.8; DB 4; Length 631;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 aaactacctaagagcta 17
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Db 168 AAAATACCAAGAGCTA 184

RESULT 15
US-09-073-587-1
Sequence 1, Application US/09073587
Patent No. 6268552
GENERAL INFORMATION:
APPLICANT: Li, Yi

TITLE OF INVENTION: Transgenic Seedless Plants
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,587
FILING DATE: 06-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,725
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Feiber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 4-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-073-587-1

Query Match 69.0%; Score 13.8; DB 4; Length 749;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 693 CTACCTATTGCTATCT 709

Search completed: September 7, 2002, 18:21:19
Job time: 28773 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:40:27 ; Search time 1139.19 Seconds
(without alignments)
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Title: US-09-834-291-1-COPY_1266_1285

Perfect score: 20

Sequence: 1 aaactactaagactatct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues 3472872

Total number of hits satisfying chosen parameters:

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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16: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT:*

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24: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	21	AA288725	Human CD95 recepto
2	20	100.0	1608	17	AAT34162	Fas promoter regio
3	17.4	87.0	1737	23	ABL11013	Drosophila melanog
4	17.4	87.0	2815	23	ABL09420	Drosophila melanog
5	17.4	87.0	3916	23	ABL11012	Drosophila melanog
6	16.8	84.0	1608	24	ABL34419	Human immune syste
7	16.8	84.0	2279	23	ABL18046	Drosophila melanog
8	16.8	84.0	6831	18	AAT80200	Phosphatidylinositol
9	16.8	84.0	6871	23	ABL10307	Drosophila melanog

10	16.8	84.0	7191	23	ABL20119	Drosophila melanog
11	16.8	84.0	17344	23	ABL20118	Drosophila melanog
12	16.8	84.0	17358	23	ABL10306	Drosophila melanog
13	15.8	79.0	1022	22	AAS47012	Human breast cancer
14	15.8	79.0	1022	22	AAS47012	Human breast cancer
15	15.8	79.0	1642	19	AAV21213	Human type II GPRH
16	15.8	79.0	2755	21	AA09173	Human znp1 (ribon)
17	15.8	79.0	2864	22	AAK94811	Human full-length
18	15.8	79.0	3293	23	AAS86514	DNA encoding novel
19	15.8	79.0	4663	22	AAK80489	Human immune/haema
20	15.8	79.0	6788	22	AAT26789	Human breast cancer
21	15.8	79.0	89047	22	AAK28547	Genomic fragment #
22	15.4	77.0	2526	20	AA06819	Chlamydia pneumonia
23	15.2	76.0	276	23	ABL27109	Drosophila melanog
24	15.2	76.0	447	23	ABL19509	Drosophila melanog
25	15.2	76.0	498	22	ABA53892	Human foetal liver
26	15.2	76.0	498	22	ABA23640	Probe #2106 for ge
27	15.2	76.0	498	22	AAK02157	Human brain expres
28	15.2	76.0	498	22	AAK02157	Probe #2121 for ge
29	15.2	76.0	498	22	AAI13188	Probe #2220 used t
30	15.2	76.0	498	22	AAI13534	Probe #2092 used t
31	15.2	76.0	1061	21	AA02101	Zea mays DNA fragm
32	15.2	76.0	1865	23	ABL06426	Drosophila melanog
33	15.2	76.0	2276	23	ABL27108	Drosophila melanog
34	15.2	76.0	2328	22	ABA14997	Human nervous syst
35	15.2	76.0	2447	23	ABL19508	Drosophila melanog
36	15.2	76.0	2918	23	ABL25058	Drosophila melanog
37	15.2	76.0	2922	22	AAK94738	Human full-length
38	15.2	76.0	3262	21	AAA98383	Human regulation f
39	15.2	76.0	5945	24	ABL33085	Human immune syste
40	15.2	76.0	6012	24	ABL34564	Human metastasis a
41	15.2	76.0	6204	22	AAS45482	Chemically pretrea
42	15.2	76.0	6204	24	ABL34003	Human immune syste
43	15.2	76.0	6357	24	ABL32096	Human immune syste
44	15.2	76.0	12304	22	ABA07882	Human ovarian and
45	15.2	76.0	12304	22	AAI03699	Human reproductive

ALIGNMENTS

RESULT 1

ID AA288725 standard: DNA; 20 BP.

XX AA288725;

AC

DT 11-MAY-2000 (first entry)

XX

DE Human CD95 receptor promoter DNA p53 binding fragment #3.

XX

XX p53; CD95 receptor; human; screening; apoptosis-modulation;

KW cancer chemotherapy; ss.

KM

OS Homo sapiens.

XX

XX DE19847779-Cl.

PN

PD 03-FEB-2000.

XX

XX 16-OCT-1998; 98DE-1047779.

PF

XX 16-OCT-1998; 98DE-1047779.

PR

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA

XX Krammer P, Mueller-Schilling M, Oren M;

PI

XX WPI; 2000-162245/15.

DR

XX Novel receptor DNA useful for identifying apoptosis-modulating

PT substances potentially useful for cancer chemotherapy

XX

PS Claim 2; Fig 5; 12pp; German.

CC This invention describes a novel p53-binding region of a human CD95
 CC receptor DNA molecule. The p53-binding region, or a vector containing
 CC it, can be used to screen for apoptosis-modulating substances
 CC potentially useful for cancer chemotherapy. This sequence represents a
 CC fragment of the human CD95 receptor promoter which is capable of
 CC binding p53.

XX Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 20; DB 21; Length 20;
 Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 aactacctagaagctatct 20
 Db 1 aactacctagaagctatct 20

RESULT 2

AAT34162 AAT34162 standard; DNA; 1608 BP.

XX AAT34162;

XX 22-0CT-1996 (first entry)

XX Fas promoter region.

XX Fas gene promoter; apoptosis; aging; autoimmune disease;
 KM T-cell senescence; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

1..1074

/*tag= a

/note= "Fas gene promoter region"

147..151

/*tag= b

/note= "Claim 7"

168..174

/*tag= c

/function= EBP20 transcription factor binding site

272..276

/*tag= d

/function= Myb transcription factor binding site

349..353

/*tag= e

/function= NF-Y transcription factor binding site

521..525

/*tag= f

/function= GF-1 transcription factor binding site

604..609

/note= "Claim 7"

621..626

/*tag= g

/function= NF-Y transcription factor binding site

1037..1043

/*tag= h

/function= AP-1 transcription factor binding site

1075..1476

/*tag= i

/function= CP2 transcription factor binding site

1075..1476

/codon_start=1479..1469
 /product= Fas protein leader
 1497..1608
 /*tag= j
 /note= "5' end of Intron 1 (full length approx.
 14 kb"

MO9622370-A1.

25-JUL-1996.

19-JAN-1996; 96WO-US00606.

20-JAN-1995; 95US-0377522.

(UABR-) UAB RES FOUND.

Cheng J, Koopman WJ, Liu C, Mountz JD, Zhou T;

WPI; 1996-354527/35.

P-PsDB; AAR99471.

Human Fas gene promoter region - used for heterologous protein
 expression and for developing products for treating Fas-mediated
 apoptosis disorders

Claim 11; Fig 2; 123pp; English.

A novel DNA segment (AAT34162) has an isolated sequence region
 defined as the Fas gene promoter region. This includes a number
 of transcription factor binding sites. A coding sequence for
 the N-terminal portion (AAR99471) of the Fas protein leader peptide
 is also included. The DNA segment was isolated from a human
 placental DNA library using a 32P-labeled segment of human Fas cDNA
 corresponding to nt 23-346. It can be combined with a structural
 gene so that the gene is under the transcriptional control of the
 transcription factor binding sites. The promoter region can be used
 to regulate Fas gene expression, e.g. in tumour or immune cells, as
 a means of treating Fas-mediated apoptosis disorders such as
 malignancies and autoimmune diseases.

Sequence 1608 BP; 398 A; 421 C; 423 G; 366 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 20; DB 17; Length 1608;
 Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aactacctagaagctatct 20

Db 507 aactacctagaagctatct 526

RESULT 3

ABLI1013 ABLI1013 standard; cDNA; 1737 BP.

XX ABLI1013;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide seq ID NO 27521.

XX Drosophila: developmental biology; cell signalling; insecticide;

XX pharmaceutical; gene; ss.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EW;
XX
DR MPI; 2001-656860/75.
XX
DR P-PSDB; ABB66910.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
PS Claim 1; SEQ ID NO 27521; 21bp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1737 BP; 446 A; 460 C; 475 G; 356 T; 0 other;
XX
Query Match 87.0%; Score 17.4; DB 23; Length 1737;
Best Local Similarity 94.7%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 aaactacctaaagctatc 19
XXXXXXXXXXXXXXXXXXXX
DB 1576 aaactacctaaagctatc 1594
XXXXXXXXXXXXXXXXXXXX
RESULT 4
AB109420/c
ID ABL09420 standard; cDNA; 2815 BP.
XX
AC ABL09420;
XX
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22742.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX
XX MPI; 2001-656860/75.
XX
XX P-PSDB; ABB65317.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 22742; 21bp + Sequence Listing; English.
PS
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2815 BP; 653 A; 671 C; 708 G; 783 T; 0 other;
XX
Query Match 87.0%; Score 17.4; DB 23; Length 2815;
Best Local Similarity 94.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 aaactacctaaagctatc 19
XXXXXXXXXXXXXXXXXXXX
DB 2076 AAACATCCCAAGAGCTATC 2058
XXXXXXXXXXXXXXXXXXXX
RESULT 5
AB11012/c
ID ABL11012 standard; cDNA; 3916 BP.
XX
XX ABL11012;
XX
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27518.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX
XX MPI; 2001-656860/75.
XX
XX P-PSDB; ABB66909.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 27518; 21bp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins

CC (AB57737-AB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 3916 BP; 1026 A; 965 C; 927 G; 998 T; 0 other;

Query Match 87.0%; Score 17.4; DB 23; Length 3916;
Best Local Similarity 94.7%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 aaactactaagagctatc 19
|||||
DB 1162 AAACCTACCCAGAGCTATC 1144

RESULT 6
ABL34419/C
ID ABL34419 standard; DNA: 1608 BP.
XX
AC ABL34419;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 2392.
XX

Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antihaemic; cytosolic; neotropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
XX Homo sapiens.
XX
OS
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EP16-) EP16NOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WP1; 2002-130909/17.

Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
XX

Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.

XX Sequence 1608 BP; 366 A; 51 C; 421 G; 770 T; 0 other;

Query Match 84.0%; Score 16.8; DB 24; Length 1608;
Best Local Similarity 90.0%; Pred. No. 27;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 aaactactaagagctatc 20
|||||
DB 1102 AAACCTACCTAAACTATCT 1083

RESULT 7
ABL18046
ID ABL18046 standard; DNA: 2279 BP.
XX
AC ABL18046;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5611.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
WP1; 2001-656860/75.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX

Claim 1; SEQ ID NO 5611; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL1840-ABL16175), expressed DNA
XX sequences (AB57737-AB72072).
XX
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX

Sequence 2279 BP; 751 A; 417 C; 442 G; 669 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 2279;
Best Local Similarity 90.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 aaactactaagagctatc 20
|||||
DB 622 aaactactaagagctatc 641

RESULT 8
AAT80200
ID AAT80200 standard; CDNA: 6831 BP.
XX
AC AAT80200;
XX

DT 22-JUN-1998 (first entry)
 XX Phosphatidylinositol 3-kinase cdk cDNA.
 DE Phosphatidylinositol 3-kinase; signal transduction; cell cycle;
 XX antagonist; inflammatory joint disease; cell proliferation; cancer;
 KW psoriasis; restenosis; atherosclerosis; therapy; diagnosis; cpk; ss.
 XX Drosophila melanogaster.
 OS
 XX Key Location/Qualifiers
 FH 148..5778
 FT CDS /*tag= a
 FT
 PN WO9731650-A1.
 XX
 XX 04-SEP-1997.
 PD
 XX 12-FEB-1997; 97WO-US02193.
 PF
 XX 29-FEB-1996; 96US-0609049.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 PI Chen Y, Molz L, Williams LT;
 DR WPI; 1997-448442/41.
 DR P-PSDB; AAW38757.
 XX
 XX New isolated phosphatidylinositol-3 kinase polypeptide - used to
 PT develop products for diagnosis and therapy, particularly for
 PT proliferative disorders, e.g. inflammatory joint diseases, or cancer
 XX
 XX Example 1; Fig 9; 77pp; English.
 XX
 CC This cDNA sequence codes for cpk (see AAW38757), a Drosophila
 CC polypeptide that belongs to a novel class of phosphatidylinositol
 CC 3-kinases that contain a C2 domain, are capable of phosphorylating
 CC a D3 hydroxyl of an inositol ring in phosphatidylinositol and
 CC phosphatidylinositol 4-phosphate, but not in phosphatidylinositol
 CC 4,5-bisphosphate, and which are involved in cell signalling cascades
 CC that control e.g. cell cycle progression and intracellular protein
 CC sorting. Short fragments of cpk cDNA were obtained from a
 CC Drosophila cDNA library by PCR (see AAW80195-96). These short
 CC fragments were used to screen the cDNA library to obtain larger
 CC fragments, and missing 5' ends were obtained by RACE. A
 CC recombinant host cell, transfected with a vector comprising a cpk
 CC nucleic acid is claimed. Novel phosphatidylinositol 3-kinases
 CC can be used to screen for agonists/antagonists of activity and
 CC in a growth method of treating a disorder caused by dysregulation
 CC of a growth factor activation signalling cascade. Antagonists
 CC may reduce Ras activation allowing treatment of proliferative
 CC disorders such as atherosclerosis, inflammatory joint disease,
 CC psoriasis, restenosis following angioplasty, and cancer.
 XX
 SQ Sequence 6831 BP; 1829 A; 1685 C; 1669 G; 1648 T; 0 other;
 XX
 XX Query Match 84.0%; Score 16.8; DB 18; Length 6831;
 XX Best Local Similarity 90.0%; Pred. No. 31;
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 aaactacctaagactatct 20
 DB 6690 aaactacctaagactatct 6709
 XX
 XX RESULT 9
 XX ABL10307 standard; cDNA; 6871 BP.
 XX
 XX AC ABL10307;
 XX
 XX

DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 25403.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 KW
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR P-PSDB; ABB66204.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Claim 1; SEQ ID NO 25403; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB57737-AB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 6871 BP; 1830 A; 1690 C; 1669 G; 1682 T; 0 other;
 XX
 XX Query Match 84.0%; Score 16.8; DB 23; Length 6871;
 XX Best Local Similarity 90.0%; Pred. No. 31;
 XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 aaactacctaagactatct 20
 DB 6731 aaactacctaagactatct 6750
 XX
 XX RESULT 10
 XX ABL20119 standard; DNA; 7191 BP.
 XX
 XX AC ABL20119;
 XX
 XX 26-MAR-2002 (first entry)
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11830.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD

XX 23-MAR-2001; 2001WO-US09231.
PF 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
CC
PS Claim 1; SEQ ID NO 11830; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 7191 BP; 1931 A; 1730 C; 1740 G; 1790 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 7191;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 aaactactaagactatct 20
D 7051 aaactactaagactatct 7070

RESULT 11
ID ABL20118 standard; DNA; 17344 BP.
XX
AC ABL20118;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11827.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 11827; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 17344 BP; 4659 A; 3886 C; 3857 G; 4942 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 17344;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 aaactactaagactatct 20
D 16204 aaactactaagactatct 16223

RESULT 12
ID ABL10306 standard; CDNA; 17358 BP.
XX
AC ABL10306;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25400.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB66203.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
CC
PS Claim 1; SEQ ID NO 25400; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins

CC (AB57737-AB872072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
XX
S0 Sequence 17358 BP; 4664 A; 3890 C; 3861 G; 4943 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 17358;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 aactacctaagcctatct 20
Db 16218 aactacctaagcctatct 16237
|||||

RESULT 13
ID AAS47012 standard; cDNA; 1022 BP.
XX AAS47012;
AC
XX 18-DEC-2001 (first entry)
DT
XX Human breast cancer CDNA clone B725P.
DE
XX Human; ss; breast cancer protein; tumour; cancer; cytostatic;
KW gene therapy.
XX
XX Homo sapiens.
OS
XX WO200179286-A2.
PN
XX 25-OCT-2001.
PD
XX 12-APR-2001; 2001WO-US12164.
PF
XX 17-APR-2000; 2000US-0551621.
PR 08-JUN-2000; 2000US-0590751.
PR 22-JUN-2000; 2000US-0604287.
PR 20-JUL-2000; 2000US-0620405.
XX
XX (CORI-) CORIXA CORP.
PA
XX
PI Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
XX WPI; 2001-611721/70.
DR
XX Breast Tumour Proteins and nucleic acids useful for the prevention,
PT diagnosis and treatment of breast cancer -
XX
XX Claim 1; Page 165; 297pp; English.
PS
XX
XX The invention relates to isolated breast tumour proteins and
CC nucleic acids that encode them, including immunogenic fragments of the
CC proteins. Also included are expression vectors expressing the
CC proteins, transformed cells and antibodies raised against the proteins or
CC an antigen presenting cell expressing the protein. The proteins and
CC nucleic acids may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate breast tumour protein expression,
CC i.e. breast tumours and breast cancer e.g. by gene therapy. The nucleic
CC acids and their complements may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids in
CC samples, and therefore which patients may be in need of restorative
CC therapy. The proteins, nucleic acids and antibodies may be used in assays
CC to identify modulators (e.g. antagonists) of breast tumour protein
CC expression and activity. The antibodies and antagonists may also be used
CC to down regulate expression and activity. The antibodies may also be used
CC as diagnostic agents for detecting the presence of the proteins in
CC samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other
CC immuno-purification diagnostic techniques. The present sequence is
CC a CDNA from a breast tumour CDNA library isolated by subtractive

CC hybridisation against a normal breast CDNA library.
XX
XX
S0 Sequence 1022 BP; 254 A; 262 C; 210 G; 296 T; 0 other;

Query Match 79.0%; Score 15.8; DB 22; Length 1022;
Best Local Similarity 89.5%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aactacctaagcctatct 20
Db 539 aactacctaagcctatct 557
|||||

RESULT 14
ID AAF17582 standard; cDNA; 1022 BP.
XX AAF17582
AC
XX AAF17582;
DT
XX 13-MAR-2001 (first entry)
DT
XX Human breast cancer associated B725P coding sequence.
DE
XX Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.
KW
XX Homo sapiens.
OS
XX WO200060076-A2.
PN
XX 12-OCT-2000.
PD
XX 15-FEB-2000; 2000WO-US05308.
PF
XX 02-APR-1999; 99US-0285480.
PR 23-JUN-1999; 99US-0339338.
PR 02-SEP-1999; 99US-0389681.
PR 03-NOV-1999; 99US-0433826.
XX
XX (CORI-) CORIXA CORP.
PA
XX
PI Yuguu J, Dillon DC, Mitcham JL, Xu J, Harlocker SL;
XX WPI; 2001-122627/13.
DR
XX
XX An isolated polypeptide useful for the treatment and diagnosis of
PT tumors e.g. breast cancer comprises at least an immunogenic portion of
PT a breast tumor protein -
XX
XX Claim 6; Page 105-106; 238pp; English.
PS
XX
XX The present invention provides the coding sequences and some protein
CC sequences of proteins associated with breast cancer in humans. These
CC sequences can be used in the diagnosis and treatment of cancers,
CC particularly breast tumours.
CC
XX
S0 Sequence 1022 BP; 254 A; 262 C; 210 G; 296 T; 0 other;

Query Match 79.0%; Score 15.8; DB 22; Length 1022;
Best Local Similarity 89.5%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 aactacctaagcctatct 20
Db 539 aactacctaagcctatct 557
|||||

RESULT 15
ID AAV21213 standard; DNA; 1642 BP.
XX AAV21213;
AC AAV21213;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:23:45 ; Search time 12179.2 Seconds
(without alignments)
34.364 Million cell updates/sec

Title: US-09-834-291-1_COPY_1266_1285

Perfect score: 20

Sequence: 1 aaactacctaagagctatct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	20	100.0	20	5	AX026104	AX026104 Sequence
2	20	100.0	40	6	AX026110	AX026110 Sequence
3	20	100.0	40	6	AX026118	AX026118 Sequence
4	20	100.0	1608	9	HSEFASX1	X82279 H.sapiens F
5	20	100.0	1877	9	HSAPT1	X81335 H.sapiens A
6	20	100.0	2165	9	HUMFAS	D31968 Human DNA f
7	20	100.0	2244	9	HSCD955FR	X87625 H.sapiens C
8	20	100.0	2380	6	AX026091	AX026091 Sequence
9	20	100.0	2827	6	AX026092	AX026092 Sequence
10	20	100.0	3212	6	AX026089	AX026089 Sequence
11	20	100.0	187313	2	AL157394	AL157394 Human DNA
12	19	95.0	172269	2	AC106508	AC106508 Rattus no
13	19	95.0	245997	2	AC093360	AC093360 Mus muscu
14	17.4	87.0	1814	3	AY051836	AY051836 Drosophila
15	17.4	87.0	154771	3	AC009214	AC009214 Drosophila
16	17.4	87.0	165283	3	AC005711	AC005711 Drosophila
17	17.4	87.0	165412	2	AC010811	AC010811 Homo sapi
18	17.4	87.0	170195	9	AC025452	AC025452 Homo sapi
19	17.4	87.0	184506	2	AC009448	AC009448 Homo sapi
20	17.4	87.0	185070	2	AC087279	AC087279 Homo sapi
21	17.4	87.0	207821	2	AC092258	AC092258 Mus muscu
22	17.4	87.0	245803	3	AE003636	AE003636 Drosophila
23	17.4	87.0	250968	2	AC014140	AC014140 Drosophila
24	16.8	84.0	526	11	G61139	AX026105 Sequence
25	16.8	84.0	1608	6	AX347321	AX347321 Sequence
26	16.8	84.0	5737	1	AF143911	AF143911 Mycoplasma
27	16.8	84.0	6831	3	DM052192	U52192 Drosophila
28	16.8	84.0	6831	6	AR072895	AR072895 Sequence
29	16.8	84.0	6831	6	AR170087	AR170087 Sequence
30	16.8	84.0	7060	1	AF143912	AF143912 Mycoplasma
31	16.8	84.0	7215	3	DMP13K6BD	X92892 D.melanogas
32	16.8	84.0	12083	1	MP059896	U59896 Mycoplasma
33	16.8	84.0	16249	1	AE000051	AE000051 Mycoplasma
34	16.8	84.0	22183	2	AC014957	AC014957 Drosophila
35	16.8	84.0	36787	2	AC023619	AC023619 Mus muscu
36	16.8	84.0	57257	2	AC109308	AC109308 Mus muscu
37	16.8	84.0	59411	9	AC004040	AC004040 Homo sapi
38	16.8	84.0	73900	9	AC092484	AC092484 Homo sapi
39	16.8	84.0	74874	2	AC097666	AC097666 Rattus no
40	16.8	84.0	81672	8	AB020755	AB020755 Arabidops
41	16.8	84.0	84504	9	AF001051	AF001051 Homo sapi
42	16.8	84.0	92948	8	AF000657	AF000657 Arabidops
43	16.8	84.0	110000	2	AC003656_6	Continuation (7 of
44	16.8	84.0	137670	2	AC025616	AC025616 Homo sapi
45						

ALIGNMENTS

RESULT	1	20 bp	DNA	linear	PAT 16-SEP-2000
AX026104	AX026104	Sequence 16 from Patent DE19847779.			
LOCUS	AX026104				
DEFINITION	AX026104				
ACCESSION	AX026104.1	GI:10187535			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	human.				

REFERENCE
AUTHORS Mueller-Schilling M., Krammer P. and Oren M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 16 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source Location/Qualifiers
1. 20
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 8 a 5 c 2 g 5 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 1 AAACCTACCTAAGAGCTATCT 20

RESULT 2
LOCUS AX026110 40 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 22 from Patent DE19847779.
ACCESSION AX026110
VERSION AX026110.1 GI:10187541
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
        substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 22 03-FEB-2000;
        DEUTSCHES KREBSFORSCH (DE)
FEATURES
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BASE COUNT 14 a 11 c 4 g 11 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 11 AAACCTACCTAAGAGCTATCT 30

RESULT 3
LOCUS AX026118 40 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 30 from Patent DE19847779.
ACCESSION AX026118
VERSION AX026118.1 GI:10187549
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
        substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 30 03-FEB-2000;
        DEUTSCHES KREBSFORSCH (DE)
FEATURES
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            /db_xref="taxon:9606"
BASE COUNT 14 a 11 c 4 g 11 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
    |||||||
Db 11 AAACCTACCTAAGAGCTATCT 30

RESULT 3
LOCUS AX026118 40 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 30 from Patent DE19847779.
ACCESSION AX026118
VERSION AX026118.1 GI:10187549
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
        substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 30 03-FEB-2000;
        DEUTSCHES KREBSFORSCH (DE)
FEATURES
    source 1..40
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT 14 a 11 c 4 g 11 t
ORIGIN

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QY 1 aaactacctaagagctatct 20
    |||||||
Db 11 AAACCTACCTAAGAGCTATCT 30

RESULT 4
LOCUS HSFASX1 1608 bp DNA linear PRI 17-FEB-1995
DEFINITION H.sapiens Fas, Apo-1 gene (promoter and exon 1).
ACCESSION X82279
VERSION X82279.1 GI:673405
KEYWORDS APO-1 gene; Fas gene.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1608)
AUTHORS Cheng,J., Liu,C., Koopman,W.J. and Mountz,J.D.
TITLE Characterization of human Fas gene. Exon/Intron organization and
        promoter region
JOURNAL J. Immunol. 154 (3), 1239-1245 (1995)
MEDLINE 95123075
REFERENCE 2 (bases 1 to 1608)
AUTHORS Cheng,J.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1994) J. Cheng, Univ. of Alabama at Birmingham,
        Univ. of Alabama, 701 South 19th street, UAB Station, LHRB 473,
        Birmingham, AL 35294-0007, USA
        Related sequences: M67454 and X63717.
FEATURES
    source 1..1608
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            /db_xref="taxon:9606"
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            /map="10q23 or 10q24.1"
            /gene="Fas, Apo-1"
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BASE COUNT 398 a 421 c 423 g 366 t
ORIGIN

Query Match      100.0%; Score 20; DB 9; Length 1608;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
    |||||||
Db 507 AAACCTACCTAAGAGCTATCT 526

RESULT 5
LOCUS HSAFPI 1877 bp DNA linear PRI 08-JUN-1995
DEFINITION H.sapiens APT gene, exon 1.
ACCESSION X81335
VERSION X81335.1 GI:537410
KEYWORDS APO-1 gene; apt gene.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1877)
AUTHORS Behnmann,I., Walczak,H. and Krammer,P.H.
TITLE Structure of the human APO-1 gene
JOURNAL Eur. J. Immunol. 24 (12), 3057-3062 (1994)
MEDLINE 95104292
REFERENCE 2 (bases 1 to 1877)
AUTHORS Krammer,P.H.
TITLE Direct Submission

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/product="Fas antigen"
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/db_xref="GI:4433150"
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1814..>2165
/number=1

BASE COUNT 508 a 555 c 555 g 547 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2165;
Best Local Similarity 100.0%; Pred. No. 7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
|||||
Db 821 AAACCTACCTAAGAGCTATCT 840

RESULT 7
HSCD955FR 2344 bp DNA
LOCUS H.sapiens CD95 gene 5' flanking region.
DEFINITION X87625
ACCESSION X87625.1 GI:902311
VERSION beta interferon; CD95 gene; silencer.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2344)
AUTHORS Rudert,F., Visser,E., Forbes,L., Lindridge,E., Wang,Y. and
Watson,J.
TITLE Identification of a silencer, enhancer, and basal promoter region
in the human CD95 (Fas/APO-1) gene
JOURNAL DNA Cell Biol. 14 (11), 931-937 (1995)
MEDLINE 96069539
REFERENCE 2 (bases 1 to 2344)
AUTHORS Rudert,F.H.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1995) F.H. Rudert, Genesis Research &
Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND
COMMENT Overlaps with X81335, & X82279-X82286.
FEATURES
source Location/Qualifiers
1..2344
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
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/map="q24.1"
564..1337
/note="silencer"
717..801
/note="beta interferon silencer B motifs"
misc_signal complement(1237..1244)
misc_signal /note="lysozyme silencer 1"
enhancer 1338..1919
promoter 1920..2344
BASE COUNT 637 a 546 c 511 g 650 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2344;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
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Db 1384 AAACCTACCTAAGAGCTATCT 1403

RESULT 8
AX026091 2380 bp DNA
LOCUS Sequence 3 from Patent DE19847779.
DEFINITION AX026091
ACCESSION AX026091
VERSION AX026091.1 GI:10187522
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2380)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 3 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source Location/Qualifiers
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BASE COUNT 579 a 595 c 568 g 638 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2380;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
|||||
Db 820 AAACCTACCTAAGAGCTATCT 839

RESULT 9
AX026092 2827 bp DNA
LOCUS Sequence 4 from Patent DE19847779.
DEFINITION AX026092
ACCESSION AX026092
VERSION AX026092.1 GI:10187523
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2827)
AUTHORS Mueller-Schilling,M., Krammer,P. and Oren,M.
TITLE Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
JOURNAL Patent: DE 19847779-C 4 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
FEATURES
source Location/Qualifiers
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BASE COUNT 728 a 676 c 657 g 766 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aaactacctaagagctatct 20
|||||
Db 1267 AAACCTACCTAAGAGCTATCT 1286

RESULT 10
AX026089 3212 bp DNA
LOCUS Sequence 1 from Patent DE19847779.
DEFINITION AX026089
ACCESSION AX026089

VERSION	AX026089.1	GI:10187520
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 3212)	
JOURNAL	Mueller-Schilling,M., Krammer,P. and Oren,M. Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 1 03-FEB-2000.	
FEATURES	DEUTSCHE KREBSFORSCH (DE) location/Qualifiers	
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Best Local Similarity	100.0%; Pred. No. 6.3;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1266 AAACCTCCTAAGACTACTT 1285	
RESULT 11		
AL157394	187313 bp DNA linear PRI 22-AUG-2001	
LOCUS	Human DNA sequence from clone RP11-399019 on chromosome 10, complete sequence.	
DEFINITION	AL157394	
ACCESSION	AL157394.15 GI:15384622	
VERSION	HNC.	
KEYWORDS	human.	
SOURCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 187313) Blakey,S. Direct Submission Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hnmquerry@sanger.ac.uk requests: clonerquest@sanger.ac.uk On Aug 31, 2001 this sequence version replaced gi:14161146. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WormPeP; Information on the WormPeP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see: http://www.chori.org/bacpac/home.htm	
COMMENT		

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FEATURES
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            100157 . 100198
            /note="Sequence confirmed by AC015461 sequenced by WtBR."
            105808 . 105972
            /note="Sequence confirmed by WtBR."
            105973 . 105989
            /note="Sequence confirmed by AC015461 sequenced by WtBR."
BASE COUNT      55669 a   36398 c   36888 g   58358 t
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy       1 aaactacctagaagctatcct 20
|||||
Db 143235 AAACACTCAAGAGCTACTT 143254

RESULT 12
LOCUS     AC106508/c
DEFINITION Rattus norvegicus clone CH230-205114, *** SEQUENCING IN PROGRESS
VERSION   AC106508
KEYWORDS
SOURCE    ORGANISM
           Rattus norvegicus
           Eumetazoa; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
           rats.
           1 (bases 1 to 172269)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alldbrooks,S.L., Amaralunne,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Blmage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowle,S., Bivleva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C.,
Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Day-Carroll,L., Dedereich,D.A., Delaney,K.R., Draper,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthevalte,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferriguto,D., Flagg,N., Ford,J.,
Foister,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Hollway,C.,
Hollins,B., Homsi,F., Howard,S., Huber,J., Huilyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolyvet,S.,
Joudah,S., Kallison,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Krivotvich,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loutseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokwenkwu,S.,

```

Okun, M., Okunonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshart, N.,
Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, R.,
Tang, H., Tansley, J., Taylor, C., Taylor, T., Tellford, B., Thomas, L.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Washington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 172269)
Morley, K. C.
Direct Submission
Submitted (12-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc.help@bcm.tmc.edu

Project Information
Center project name: GLAZ
Center clone name: CH230-205114

Summary Statistics
Assembly program: Phrap; version 0.990329first call to
findphraplist

Consensus quality: 145908 bases at least Q40
Consensus quality: 152564 bases at least Q30
Consensus quality: 158487 bases at least Q20
Estimated insert size: 150457; sum-of-coverage estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 2.7x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 54 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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7929: contig of 7929 bp in length
7930: gap of unknown length
8030: contig of 7846 bp in length
15876: gap of unknown length
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22988: gap of unknown length
23088: contig of 6112 bp in length
29200: gap of unknown length
29200: contig of 5553 bp in length
34853: gap of unknown length
34853: contig of 6896 bp in length
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47071: gap of unknown length
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55244: gap of unknown length
55244: contig of 4192 bp in length
59535: gap of unknown length
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63661: gap of unknown length
63661: contig of 3809 bp in length
67570: gap of unknown length
67570: contig of 5119 bp in length

72789: gap of unknown length
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75893: gap of unknown length
75992: contig of 3145 bp in length
79138: gap of unknown length
79237: contig of 5240 bp in length
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88642: gap of unknown length
88742: contig of 2634 bp in length
91376: gap of unknown length
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95027: gap of unknown length
95126: contig of 3336 bp in length
99062: gap of unknown length
99162: contig of 3719 bp in length
99163: gap of unknown length
102881: contig of 3783 bp in length
102982: gap of unknown length
106764: contig of 3038 bp in length
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109903: gap of unknown length
110002: contig of 2517 bp in length
110003: gap of unknown length
112519: contig of 3007 bp in length
112620: gap of unknown length
115626: contig of 3293 bp in length
115728: gap of unknown length
119019: contig of 1782 bp in length
119020: gap of unknown length
119119: contig of 2642 bp in length
120901: gap of unknown length
120902: contig of 1524 bp in length
121002: gap of unknown length
123644: contig of 2727 bp in length
123744: gap of unknown length
125268: contig of 2976 bp in length
125368: gap of unknown length
128095: contig of 1712 bp in length
128194: gap of unknown length
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132125: gap of unknown length
132126: contig of 1365 bp in length
135571: gap of unknown length
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138177: gap of unknown length
138178: contig of 149768 bp in length
138278: gap of unknown length
141253: contig of 1075 bp in length
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141354: contig of 1595 bp in length
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143066: contig of 1572 bp in length
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145348: gap of unknown length
145348: contig of 1572 bp in length
146713: gap of unknown length
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159070: contig of 1572 bp in length
161597: gap of unknown length
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163410: gap of unknown length
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164698: gap of unknown length
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164799: gap of unknown length
164799: contig of 1572 bp in length
166167: gap of unknown length
166167: contig of 1572 bp in length
166267: gap of unknown length
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FEATURES
source
1. 172269
Location/Qualifiers
/db_xref="taxon:10116"
/db_xref="CH230-205114"
/db_xref="Rattus norvegicus"
BASE COUNT 48455 a 35040 c 34181 g 49053 t 5540 others

Query Match
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aactactaagactatct 20
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Db 121229 AACTACTAAGACTATCT 121211

RESULT 13
AC093360 245997 bp DNA linear HTG 20-AUG-2001
LOCUS Mus musculus clone RP23-57F18, WORKING DRAFT SEQUENCE, 7 unordered
DEFINITION pieces.
AC093360
AC093360.1 GI:15213905
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP;
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 245997)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
2 (bases 1 to 245997)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B.,
Brown,A., Camarata,J., Campoliano,A., Chang,J., Chazaro,B.,
Chopel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearliano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heatord,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Lacroque,K.,
Lamaze,R., Lander,T., Lehoczy,J., Levine,N., Matthews,C.,
Maclean,C., Macdonald,P., Major,J., Margus,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrum,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norman,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Piere,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnapack,R.,
Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Teffaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-AUG-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR

Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L14296
Center clone name: 57_F_18
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 242847 bases at least Q40
Consensus quality: 244315 bases at least Q30
Consensus quality: 244906 bases at least Q20
Insert size: 25000; agarose-fp
Insert size: 245397; sum-of-coverage
Quality coverage: 9.9 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 9345 9444: gap of 100 bp
* 9445 13083: contig of 3639 bp in length
* 13084 13183: gap of 100 bp
* 13184 15745: contig of 2562 bp in length
* 15746 15845: gap of 100 bp
* 15846 20539: contig of 4694 bp in length
* 20540 20639: gap of 100 bp
* 20640 62896: contig of 42257 bp in length
* 62897 62996: gap of 100 bp
* 62997 193684: contig of 130688 bp in length
* 193685 193784: gap of 100 bp
* 193785 245997: contig of 52213 bp in length.
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/db_xref="taxon:10090"
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13184..15745
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15846..20539
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20640..62896
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62997..193684
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193785..245997
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vector_side:right"
BASE COUNT 73285 a 49514 c 49348 g 73250 t 600 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 aactactaagactatct 20
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Db 232480 AACTACTAAGACTATCT 232498

RESULT 14
AY051836 1814 bp mRNA linear INV 27-AUG-2001
LOCUS Drosophila melanogaster LD33880 full length cDNA.
ACCESSION AY051836
VERSION AY051836.1 GI:15291982
KEYWORDS FLI,CDNA.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1814)
Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,
Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanavong,S., Wan,K.,
Yu,C., Lewis,S.E., Rubin,G.M. and Celniker,S.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
COMMENT Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES
Source
1. .1814
Location/Qualifiers
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/strain="y: cn bw sp"
/db_xref="taxon:7227"
/map="33D5-33E1"
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/gene="CG6388"
/note="alignment with genomic scaffold AE003636"
/db_xref="FLYBASE:FBgn0032430"
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/note="Longest ORF"
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ILEALATGRLSIRYAOEIAAGYAOIVANDLSROAVASINTIRNKYEELIEPSHDA
MTLWLTSTOPEKRFPAVDLDPGCGPRFLDGMOCVLDGILLVATDMVLAAENAP
ACVAYGVSVPILMKCCEKALILHLCHISHANRYKYLIPPLISADFTIRIVRY
VGQAQCKLSMSKQSWIYQCTGCTFTLQPGITKPNPTAGNPOOLKFGIPGPAVNSQ
CEHGCHRHLLGPIISAPINHEPEVDLTLAVQETLQSIGTORRIGVIGVSMVOEELQ
DVLYPTPDKLCCLVLEIYVPMLEKRSAILHAGYRVSYSKSNKLTNAPPAVLMDI
LRSMSKRHPVNERMIPGSLAAILISCECTAVYEPELHPEANKSRKSLSRQEND
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HLPPKPLEATA"

BASE COUNT 481 a 476 c 481 g 376 t

ORIGIN
Query Match 87.0%; Score 17.4; DB 3; Length 1814;
Best Local Similarity 94.7%; Pred. NO. 1.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1585 AACTACCACAGAGCTATC 1603
Oy 1 aaactactaagactac 19
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Db 1585 AACTACCACAGAGCTATC 1603

RESULT 15
AC009214 154771 bp DNA linear INV 06-SEP-2001
LOCUS Drosophila melanogaster, chromosome 2L, region 33E-33F, BAC clone
DEFINITION BACRO5E09, complete sequence.
ACCESSION AC009214
VERSION AC009214.7 GI:15451504
KEYWORDS HTG.
SOURCE Drosophila melanogaster
fruit fly.
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 154771)
Celniker,S.E., Adams,M.D., Krommiller,B., Tyler,D., Wan,K.H.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Bazom,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
Fieriera,S., Frise,E., Galle,R.F., Gary,N.S., George,R.A.,
Gonzalez,M., Hovick,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Idegam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
Mortosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanavong,S., Piltman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Svirskaas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
TITLE Sequencing of Drosophila chromosome 2L, region 33E-33F
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 154771)
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazek,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Humastli,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequerra,A., Sethi,H., Snir,E.,
Svirskaas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
Rubin,G.M.
TITLE Direct Submission
JOURNAL Submitted (06-AUG-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT On Sep 6, 2001 this sequence version replaced g1.13324753.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end and sequences from a whole genome
shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive web site (http://www.fruitfly.org/sequence/) or send email
to bdg@fruitfly.berkeley.edu.

FEATURES
source
1. .154771
Location/Qualifiers
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/db_xref="taxon:7227"
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/map="33E-33F"
/clone="BACRO5E09 (D865)"

/clone.lib="RPCT-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial ECORI in
pBACE3.6)"
BASE COUNT 47347 a 29741 c 30511 g 47172 t
ORIGIN

Query Match 87.0%; Score 17.4; DB 3; Length 154771;
Best Local Similarity 94.7%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 aaactactaagaagctatc 19
||||||| |||||||
Db 663 AAACCTACCCAGAGCTATC 681

Search completed: September 7, 2002, 18:23:58
Job time: 28937 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 10:21:46 ; Search time 212.3 Seconds
(without alignments)
3716.320 Million cell updates/sec

Title: US-09-834-291-1
Perfect score: 3212
Sequence: 1 ttgagactctcagaataatg.....ttgcagatgctaatcaag 3212

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/2/ina/5A.COMB.seq:*
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5: /cgn2_6/prodata/2/ina/PCTUS.COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	7.8	2551	4 US-09-290-640-1	Sequence 1, Appl
2	226	7.0	2471	1 US-08-444-231-18	Sequence 18, Appl
3	226	7.0	2471	1 US-08-152-443A-18	Sequence 18, Appl
4	226	7.0	2534	2 US-08-219-237B-1	Sequence 1, Appl
5	226	7.0	2534	4 US-08-468-560C-1	Sequence 1, Appl
6	226	7.0	2534	4 US-09-180-100-16	Sequence 16, Appl
7	79.4	2.5	7218	1 US-08-232-463-14	Sequence 14, Appl
8	67.8	2.1	7218	1 US-08-232-463-14	Sequence 14, Appl
9	59.8	1.9	35100	1 US-08-306-691B-19	Sequence 19, Appl
10	59.8	1.9	35100	5 PCT-US93-06251-19	Sequence 19, Appl
11	57	1.8	857	5 PCT-US95-17083-9	Sequence 9, Appl
12	57	1.8	920	5 PCT-US95-17083-7	Sequence 9, Appl
13	57	1.8	975	5 PCT-US95-17083-5	Sequence 9, Appl
14	57	1.8	1104	5 PCT-US95-17083-3	Sequence 3, Appl
15	57	1.8	1167	5 PCT-US95-17083-1	Sequence 3, Appl
16	51.6	1.6	556	4 US-09-018-584A-25	Sequence 25, Appl
17	50.8	1.6	370	2 US-08-332-766A-8	Sequence 8, Appl
18	50	1.6	376	2 US-08-623-906A-18	Sequence 18, Appl
19	49.8	1.6	5751	4 US-09-417-455-7	Sequence 7, Appl
20	49.8	1.6	5751	4 US-09-348-942-7	Sequence 7, Appl
21	49.2	1.5	361	4 US-09-018-584A-9	Sequence 9, Appl
22	48.4	1.5	50	2 US-08-713-557B-35	Sequence 35, Appl
23	48.4	1.5	15144	3 US-08-458-434A-6	Sequence 6, Appl
24	48	1.5	421	1 US-08-480-784-24	Sequence 24, Appl
25	48	1.5	421	1 US-08-483-553-24	Sequence 24, Appl
26	48	1.5	421	1 US-08-487-002-24	Sequence 24, Appl
27	48	1.5	421	1 US-08-483-554B-24	Sequence 24, Appl

28	48	1.5	421	1 US-08-488-011B-24	Sequence 24, Appl
29	48	1.5	421	4 US-08-850-727-24	Sequence 24, Appl
30	48	1.5	421	5 PCT-US95-10202-24	Sequence 24, Appl
31	48	1.5	421	5 PCT-US95-10203-24	Sequence 24, Appl
32	48	1.5	421	5 PCT-US95-10220-24	Sequence 2, Appl
33	47.8	1.5	5852	1 US-07-867-106-2	Sequence 27, Appl
34	47.6	1.5	287	2 US-08-332-766A-27	Sequence 11, Appl
35	47.4	1.5	1679	2 US-08-365-486A-11	Sequence 11, Appl
36	47.4	1.5	1679	4 US-08-880-342-11	Sequence 11, Appl
37	47.4	1.5	12141	4 US-09-488-671-10	Sequence 10, Appl
38	47.4	1.5	80246	4 US-09-078-294-4	Sequence 3, Appl
39	47.4	1.5	80595	4 US-09-078-294-3	Sequence 8, Appl
40	47.2	1.5	295	4 US-08-332-766A-11	Sequence 11, Appl
41	47.2	1.5	325	2 US-08-332-766A-11	Sequence 26, Appl
42	47.2	1.5	446	2 US-08-332-766A-10	Sequence 10, Appl
43	46.8	1.5	444	4 US-09-018-584A-19	Sequence 19, Appl
44	46.6	1.5	444	4 US-08-623-906A-13	Sequence 13, Appl
45	45.6	1.4	388	2 US-08-623-906A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-290-640-1
; Sequence 1, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (221)..(1228)
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 267
; ISSUE: 15
; PAGES: 10709-10715
; DATE: 1992-05-25
; DATABASE ACCESSION NUMBER: X63717/Genbank
; DATABASE ENTRY DATE: 1996-07-19
; US-09-290-640-1

Query Match 7.8%; Score 252; DB 4; Length 2551;
Best Local Similarity 100.0%; Pred. No. 5.9e+60;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 gcaaggtgacacacaggttcaaaagcctcttgaggagtgagggaagcggttaca 60

OY 2067 gtgacttgcttgagcctcagggcgaggtgacatgacagaaacacacctgaagcagcc 2126
| gtgacttgcttgagcctcagggcgaggtgacatgacagaaacacacctgaagcagcc 120
Db 61 gtgacttgcttgagcctcagggcgaggtgacatgacagaaacacacctgaagcagcc 120

OY 2127 ttgcttcccgagcgaggtgctctcttcccgcggtgtgttgacccgctgaagtgag 2186
| ttgcttcccgagcgaggtgctctcttcccgcggtgtgttgacccgctgaagtgag 180
Db 121 ttgcttcccgagcgaggtgctctcttcccgcggtgtgttgacccgctgaagtgag 180

OY 2187 ttgggaaagctcttcaactcagagagatgctcaacaacatgttgagcatctgacct 2246
| ttgggaaagctcttcaactcagagagatgctcaacaacatgttgagcatctgacct 240
Db 181 ttgggaaagctcttcaactcagagagatgctcaacaacatgttgagcatctgacct 240

OY 2247 cctacctcgt 2258
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Db 241 cctacctcgt 252

RESULT 2

US-08-444-231-18
; Sequence 18, Application US/08444231
; Patent No. 5652210
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,231
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/152,443
; FILING DATE: 15-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 195..1136
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 243
; US-08-444-231-18

Query Match 7.0%; Score 226; DB 1; Length 2471;
Best Local Similarity 100.0%; Pred. No. 9.9e-53;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 CTCGCCGGGTTGGTGAACCCGCTCAGGAGTGGGGAGCTCTTTCATCTCGAGG 180
OY 2213 attgctaacacatgctggcagctcagccctcactcgt 2258
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Db 181 ATTGCTACACACCACTGCTGGGCACTGAGCCCTCTACTCTGCT 226

RESULT 3

US-08-152-443A-18
; Sequence 18, Application US/08152443A
; Patent No. 5663070
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: SHAPIRO, JOHN P.
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,443A
; FILING DATE: 15-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 195..1136
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 243
; US-08-152-443A-18

Query Match 7.0%; Score 226; DB 1; Length 2471;
Best Local Similarity 100.0%; Pred. No. 9.9e-53;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2093 ggcactggcacgaaacacacccctgaagccagccctgctgcccagggagcgtcctt 2152
|||||
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Db 121 CTCGCCGGGTTGGTGAACCCGCTCAGGAGTGGGGAGCTCTTTCATCTCGAGG 180

QY 2213 attgctcaaacaccatctggtgcatctgagaccctcactctgt 2258
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Db 181 ATTGCTCAACACCATGCTGGCATCTGGACCTCTACCTCTGT 226

RESULT 4

US-08-219-237B-1
; Sequence 1, Application US/08219237B
; Patent No. 58/45346
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Hellwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY: pCEV4
; CLONE: clone pF58
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 195..1202
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 195..242
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 243..1199
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 1831..1836
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: polyA_site

LOCATION: 2352..2357
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 2518..2523
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
US-08-219-237B-1

Query Match 7.0%; Score 226; DB 2; Length 2534;
Best Local Similarity 100.0%; Pred No. 1e-52;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2153 cccccgaggttggtgagcccgctcagtagaggttgaggagctcttcaactcggag 2212
|||||
Db 121 CTCGCCGGGCTTGTTGGACCCGCTCAGTAGGAGTTGGGAAAGCTCTTTCACCTTGGAGG 180
QY 2213 attgctcaaacaccatctggtgcatctgagaccctcactctgt 2258
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Db 181 ATTGCTCAACACCATGCTGGCATCTGGACCTCTACCTCTGT 226

RESULT 5

US-08-468-560C-1
; Sequence 1, Application US/08468560C
; Patent No. 6270998
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,560C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR., GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 20-4393P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

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Db      61      ggcactggcacggaacacacacccctgaagccagccctgtgtgtcccaaggagggagctgcctct      120

QY      2153      ctccgcggggtgtgtgtgagaccgcctcaagtcagaaattgggggaagctcttcaactcgaag      2212
Db      121      ctccgcggggtgtgtgtgagaccgcctcaagtcagaaattgggggaagctcttcaactcgaag      180

QY      2213      atgctcaacaacacatctgtcgtggcatctgtgaacctctactctcgt      2258
Db      181      atgctcaacaacacatctgtcgtggcatctgtgaacctctactctcgt      226

RESULT      7
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
;
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFFLINGER, F.

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RESULT 7
 US-08-232-463-14
 ; Sequence 14, Application US/08232463
 ;
 ; Patent No. 5670367
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500
City: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313

APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT9gpt-Fls
US-08-232-463-14

Query Match	2.5%;	Score 79.4;	DB 1;	Length 7218;
Best Local Similarity	5.4%;	Pred. 1.3e-11;		
Matches	20;	Conservative	224;	Mismatches 125;
				Indels 0;
				Gaps 0

[illegible]

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Db 1226 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1285
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Db 1286 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1345
QY 634 atccctctccctacccctccctccctccctccctccctccctctctt 693
Db 1346 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1405
QY 694 acatttttataatgaacttcaattggaatagtttagaatcaaaaatt 753
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Db 1466 GCATAGATA 1474

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RESULT 8

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US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEITLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOMLOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)836-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpc-Fls
; US-08-232-463-14

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Query Match 2.1%; Score 67.8; DB 1; Length 7218;
Best Local Similarity 8.2%; Pred. No. 2,1e-08;
Matches 36; Conservative 227; Mismatches 174; Indels 0; Gaps 0;
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QY 926 tgggtgaagtcagtgacagatgcaaacacagaggtgtaggaagccctc 985
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QY 986 acctaacctagatttagggcccaagcgtcccaagaagaatcgaactaga 1045
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RESULT 9

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US-08-306-691B-19
; Sequence 19, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorina & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383

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TOPOLOGY: linear
PCT-US95-17083-7

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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 5, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 975 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-5

Query Match
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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 3, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-3

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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17083
; FILING DATE: CONCURRENTLY HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/371,263
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: September 7, 2002, 18:21:05
Job time: 28759 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 10:21:46 ; Search time 13836.9 Seconds
(without alignments)
5022.158 Million cell updates/sec

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Gapop 10.0 , Gapept 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3	2346.6	73.1	2837	US-09-834-291-4	Sequence 4, Appl
4	2143.4	66.7	2165	US-09-665-615B-94	Sequence 94, Appl
5	2143.4	66.7	2165	US-09-802-669-94	Sequence 94, Appl
6	1899.6	59.1	2380	US-09-834-291-3	Sequence 3, Appl
7	1536.8	47.8	1608	US-08-377-522-1	Sequence 1, Appl
8	1536.8	47.8	1608	US-08-377-522C-1	Sequence 1, Appl
9	1536.8	47.8	1608	US-08-377-522C-1	Sequence 1, Appl
10	799.8	24.9	3814	US-60-324-185-29531	Sequence 29531, A
11	713	22.2	720	US-09-834-291-2	Sequence 2, Appl
12	424.2	13.2	449	US-09-404-288-674	Sequence 674, App
13	424.2	13.2	449	US-09-524-038-674	Sequence 674, App
14	387.4	12.1	1368	US-60-324-185-9888	Sequence 9888, App
15	367.8	11.5	1732	US-09-644-861-7725	Sequence 7725, App
16	367.8	11.5	1732	US-09-652-911-10283	Sequence 10283, A
17	336.2	10.5	495	US-09-652-911-4924	Sequence 4924, Ap
18	336.2	10.5	2871	US-09-652-124-8816	Sequence 8816, Ap
19	336.2	10.5	2871	US-09-717-350-4919	Sequence 4919, Ap
20	336.2	10.5	2871	US-09-726-172-2083	Sequence 2083, Ap
21	336.2	10.5	2871	US-09-726-175-3031	Sequence 3031, Ap
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23	336.2	10.5	2871	US-09-726-810-2456	Sequence 2456, Ap
24	334.4	10.4	772	US-09-760-455-21	Sequence 21, App
25	334.4	10.4	772	US-09-760-485-327	Sequence 327, App
26	331.4	10.3	2641	US-60-172-373-13644	Sequence 13644, A
27	331.4	10.3	2641	US-60-213-360-1236	Sequence 1236, Ap
28	330.8	10.3	575	US-09-471-275-3315	Sequence 3315, Ap
29	327.4	10.2	458	US-09-306-350A-14682	Sequence 14682, A
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SUMMARIES

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C 42 292.8 9.1 1655 56 US-60-172-373-10224 Sequence 10224, A
C 43 289.8 9.0 467 56 US-60-172-360-3705 Sequence 3705, App
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ALIGNMENTS

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US-09-834-291-1
; Sequence 1, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834, 291
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; NUMBER OF SEQ ID NOS: 32
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1
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 ; APPLICANT: Engelhard, Eric
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: A-71171/RMS/DCF
 ; CURRENT APPLICATION NUMBER: US/09/997, 722
 ; CURRENT FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: US 09/747, 377
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 09/798, 586
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 301
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 45121
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-997-722-10

Query Match 99.4%; Score 3193; DB 36; Length 45121;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3207; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 tggagactctcaggaatgctgtgtaataataataacattagagatgccaactgt 60

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Db 8054 tttccccaagaacacccagatcatatagtgctcatatcatatgattcttcaagaattcca 8113
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; GENERAL INFORMATION:
 ; APPLICANT: Krammer, Peter
 ; APPLICANT: Muller-Schilling, Martina
 ; APPLICANT: Oren, Moshe
 ; TITLE OF INVENTION: p53 Binding Areas
 ; FILE REFERENCE: 4121-122
 ; CURRENT APPLICATION NUMBER: US/09/834, 291
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: PCT/DE99/03343
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: DE 198 47 779.1
 ; PRIOR FILING DATE: 1998-10-16
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 4
 ; LENGTH: 2827
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; US-09-834-291-4

Query Match 73.1%; Score 2346.6; DB 32; Length 2827;
 Best Local Similarity 87.0%; Pred. No. 0;
 Matches 2795; Conservative 0; Mismatches 24; Indels 394; Gaps 4;

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 Db 61 tttcccaagacacccagcatctttaggttctcaataagattcttcaagaagattcca 120
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Db 2188 ----- 2187
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Db 2548 gctctgtccctcccggaatctctctttaagaactgtatgcgtctgagtgatt 2607
QY 3000 cattttgtttttttctgcgcctctctcttcttctttcttgcctcttcttgctgcactc 3059
Db 2608 cattgttttcttcttccgcctctctcttcttcttcttcttgcctcttcttgactc 2667
QY 3060 ccatgtgtattctgtctgtcttccctgcgtgaggttggtgtactcgttccaccgcacag 3119
Db 2668 ccatgtgtattctgtctgtcttccctgcgtgaggttggtgtactcgttccaccgcacag 2727
QY 3120 aaccgcgcactatattgccaagaacttgcagcagcctgttttgaagaagtcctcgct 3179
Db 2728 aaccgcgcactatattgccaagaacttgcagcagcctgttttgaagaagtcctcgct 2787
QY 3180 cagaatgccagcttgcagatggtcaatacaag 3212
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RESULT 4
US-09-665-615B-94
; Sequence 94, Application US/09665615B
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-665-615B-94

Query Match 66.7%; Score 2143.4; DB 26; Length 2165;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2158; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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QY 507 gggcctataatgaataatgaataagtaagaagatccacatatgttgatgtcgtgtataaa 566
Db 61 gggcctataatgaataatgaataagtaagaagatccacatatgttgatgtcgtgtataaa 120
QY 567 ttcaactcaagagatactgatttgcgaattgttccttcccttttctctctcc 626
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QY 627 tctttcacctctcttcccttaccctctctcttcccttcccttcccttcccttccct 686
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Db 241 tcttttacaattttttatttaaaatgaacttccaatttggaaatgatttaagattcaa 300
QY 747 aaatttcagagagataataacagagaatgcacataacacatccctcttaccacttctt 806

Db 301 aaatttcagagagataataacagagaatgcacataacacatccctcttaccacttctt 360
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[illegible]

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; SEQ ID NO 94
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1782)...(1813)
US-09-802-665-94

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Query Match	66.7%	Score 2143.4	DB 31	Length 2165
Best Local Similarity	99.7%	Pred. No. 0		
Matches 2158; Conservative	0	Mismatches 6	Indels 1	Gaps 1

[illegible]

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QY	1406	tgaatgtttaataatagctgvgggtctatgtcgatttggcttaagtgttatgctttttcc	1465
Db	961	tgaatgttttaatatagctgvgggtctatgtcgatttggcttaagtgttatgctttttcc	1020
QY	1466	cttgagaaataaaaaactaaggggcccctctttcagagccttatggcgaacatctgta	1525
Db	1021	cttgagaaataaaaaactaaggggcccctctttcagagccttatggcgaacatctgta	1080
QY	1526	cttttcaatagttaactgctccatctccagaaagcgtctgagcctccatggttgagcc	1585
Db	1081	cttttcaatagttaactgctccatctccagaaagcgtctgagcctccatggttgagcc	1140
QY	1586	acaacatgacagcccgatgtcaaatgcccgcgaagtcttctctgtatgactccagcaat	1645
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QY	1646	agccaaagctccctgtfacccagagcagaccctctggtctgtagcttcatcttccitaa	1705
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QY	1706	ctctcccaacttccccaggttgaactatacagaagaagcctttaagaahggcagagagccgcg	1765
Db	1261	ctctcccaacttccccaggttgaactatacagaagaagcctttaagaahggcagagagccgcg	1320
QY	1766	tctcgaagctctccacacttgaaagtgtgagcatgcccagcactgcagagaaacgcccggagacaga	1825
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Db	1441	ccgcgcgcagagccaaagtgtgctgtaatgtgagccctccccaaccccgagcgttccccaagc	1500
QY	1946	gagagcttccctccacactccctccggaacacacggggcttttgcgtgtgctctcgtatctcg	2005
Db	1501	gagagcttccctccacactccctccggaacacacggggcttttgcgtgtgctctcgtatctcg	1560
QY	2006	cgcgaagagtgtgacacacagaagtgtgttcaaaagacgcttctcgtggagagtgtgaggaagccggtttacg	2065
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QY	2066	agtgagcttggcctgvggagccctccagggggggcgacatcgtgcacggaacacacacccctgagagccagcc	2125
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Db	1741	gtctgggggaagctctctacactctcgagagatgtgtcaacaacacatgctvggcatctggaacc	1800
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Db	1801	tctcaacgtctggtagatccctctccctcccgccgggtgaggaagcttaccgccgttctaaagcccggg	1860
QY	2306	gataagacaaagtgtgggctggggcgcgagagcgtgacgagatgtgcggccgagccagcgcgcgcgc	2365
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QY	2366	ggggcaacctggvggagcgagcgagctgtctgcggagagagcgtttgagagactgggttcccggggctgct	2425
Db	1921	ggggcaacctggvggagcgagcgagctgtctgcggagagagcgtttgagagactgggttcccggggctgct	1980

OY	2426	tagaaccttccctcaagccgggtgcctcaagaacatggaagactgtcttctctggcct	2485
Db	1981	taggaacttccctcaagccgggtgcctcaagaacatggaagactgtcttctctggcct	2040
OY	2486	tgaatgcgaagatcgtgatccgcctctggcagcgcgggcgcaagctccggcgctcctcogagacca	2545
Db	2041	tgaatgcgaagatcgtgatccgcctcctggcagcgcgggcgcaagctccggcgctcctcogagacca	2100
OY	2546	ctcgagctccacgcttgagggtggcgctggggggcgagcaagaaattgaagcggaagctctggga	2605
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RESULT 6			
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: Sequence 3, Application US/09834291			
: GENERAL INFORMATION:			
: APPLICANT: Krammer, Peter			
: APPLICANT: Muller-Schilling, Martina			
: APPLICANT: Oren, Moshe			
: TITLE OF INVENTION: p53 Binding Areas			
: FILE REFERENCE: 4121-122			
: CURRENT APPLICATION NUMBER: US/09/834,291			
: CURRENT FILING DATE: 2001-08-21			
: PRIOR APPLICATION NUMBER: PCT/DE99/03343			
: PRIOR FILING DATE: 1999-10-18			
: PRIOR APPLICATION NUMBER: DE 198 47 779.1			
: PRIOR FILING DATE: 1998-10-16			
: NUMBER OF SEQ. ID NOS: 32			
: SOFTWARE: PatentIn Ver. 2.1			
: SEQ ID NO 3			
: LENGTH: 2380			
: TYPE: DNA			
: ORGANISM: Homo Sapiens			
US-09-834-291-3			
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Best Local Similarity 84.9%; Pred. No. 0;			
Matches 2348; Conservative 0; Mismatches 24; Indels 394; Gaps			
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OY	508	ggcataatgataaatttaagtaagaagatccacatactgagttgtcgtctataat	567
Db	61	ggcataatgataaatttaagtaagaagatccacatactgagttgtcgtctataat	120
OY	568	tcaacatcaagaagatactgatttgcgaatgctccttcccttttttctctctcct	627
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OY	688	cttttacaattttttatttaataatgaactttcatttttgaaatagttttagattcaaa	747
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Db	301	aaatttgcagagataatacagagaatgccacatacactcctactatccactctttt	360
OY	808	tgtgtcattatagatcctcagagtggtgtgcacaagaagcttgcagcgccagggtcttccat	867
Db	361	tgtgtcattatagatcctcagagtggtgtgcacaagaagcttgcagcgccagggtcttccat	420

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Db 1888 gggggcggggagagagcctcagcctcagacataatgtctcaatttcttgagagtt 1947
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Db 1948 cagaacgtaagaaataagtcagcagcgaagcagtggttaagccggagggcctcgaaagaa 2007
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Db 2188 cttctctcttctgccccttctcttctgctgcaactccatccatgctgattctctgctgctctctg 2247
QY 3087 ctcgaggttggtgctgactcgtctccaccgcacagaaacccggcgccctattatgccaagaa 3146
Db 2248 ctcgaggttggtgctgactcgtctccaccgcacagaaacccggcgccctattatgccaagaa 2307
QY 3147 acttgagcagcctgttttgaagaagtcctcgtctcgaagaatgccaagcttgccaagtgtccta 3206
Db 2308 acttgagcagcctgttttgaagaagtcctcgtctcgaagaatgccaagcttgccaagtgtccta 2367
QY 3207 tcaag 3212
Db 2368 tcaag 2373

RESULT 7
US-08-377-522-1
; Sequence 1, Application US/08377522
; GENERAL INFORMATION:
; APPLICANT: Mountz, John D.
; APPLICANT: Liu, Changdan
; APPLICANT: Cheng, Jianhua
; APPLICANT: Koopman, William J.
; APPLICANT: Zhou, Tong
; TITLE OF INVENTION: Human Fas Gene Promoter Region
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,522
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Serlich, Gary J.
REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UOAB:034/SBR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
TELEX: N/A

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1467..1496
US-08-377-522-1

Query Match 47.8%; Score 1536.8; DB 7; Length 1608;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1582; Conservative 0; Mismatches 17; Indels 5; Gaps 3;

QY 767 agagaatgccataaccatccctctatcccaactcttttggctcattagatgctca 826
Db 7 ACAGAGATGCCCTATACATCTCTATCCACCTCTTTTGTCTCATATGATGCTCA 66
QY 827 gaggtgtgcaagaggttgagagcccgaggtcttcccatgagcctacaactactca 886
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Db 67 GAGTGTGTCACAAAGGCTGGCACGCCAGGCTTCTCATGCGACTACAGCTACTCA 126
QY 887 aaggtggaacagagacaagcctatcaacacctaagaactggtgtaagtgcagtgacag 946
Db 127 AAGGTGGAACAGAGACAAGCCTATCAACACCTCAAGACTGTGTGAAGTGACGTGACAG 186
QY 947 atgcaaaacacagaggtgtagaagaagccctcaggaagggttaacctaaactgaattgagggc 1006
Db 187 ATGCAAAACACAGAGGAGTAGAAGGCCCTCAGAGAGGCTAACCTAAGATTGAGAGGC 246
QY 1007 cc-aacaggctccagagaagaatgtaactgagaggaagccttaagatbaaagatgagc 1065
Db 247 CCAAAACAGGCTCCAGAAAGAAATGTCACTGAGAGAGAGCCTAAGATBAACAGTGGCC 306
QY 1066 taagcaaaagggtatataatgltgltatlaaagggtgtaactlaatlgggaaggagagag 1125
Db 307 TAAGCAAAAGGTTATTAAATGTTATTAAATGGGTGATTAATGGGAAGGAGAGAGG 366
QY 1126 ttgcagagtgaggtgtagagagctgtgtgagcagatgccaagaagtactgaaacctttagt 1185
Db 367 TTGCAGAGTGAGGTGAGAGCTTTGGAGAGATGCCAAAGAAATACGAAACCTTTAGTG 426
QY 1186 tgtccagctctggaactgcaatccaaattcaaggttcaagtaatgltcaattccaaacata 1245
Db 427 TGTCAGTCTGAGACTGTCATCCAAATTCAGGTTCAAGTAATGATGTCTATTCCAAACATA 486
QY 1246 cctctgttaaatcactgctaaactaactaagaagctactaccgttccaaagaactagt 1305
Db 487 CCTTGTGTAATTAATTCATGCTAAACTACCTAAGAGCTATACGGTTCCAAAGCAATAGTG 546
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Db 607 GGCAGGAATATATGATACGACGACGACGACGACGACGACGACGACGACGACGACGACG 666
QY 1426 ggcataagcatttgcttaagtgttagcttcttccctctctgagaataaataaactaag 1485
Db 667 GGCTATGACATTTGGCTTAAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 726
QY 1486 ggagccctccttctgaagagctatagcgcaaatcgtacttcttctatgctgactg 1545
Db 727 GGCCCTCCCTTTTCAGAGCCCTATGGCGCAACATGCTGTTTTCATATGTTAACTG 786
QY 1546 tccattccagaagaagctgtagagcctcctcatgltgcaagcaacaacatggaagccagctc 1605
Db 787 TCCATTCCAGAAACGCTGTGAGAGCTCTCATGTTGACGACCAAGATGAGACGCCACGTC 846
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Db 847 AATGCCCCGCAAGTCTTCTGAGTGAAGTCCAGCAATTAAGCCAAAGGCTCTGTACCA 906
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QY 1726 gaactacagcagaagcctttagaagaagcgagagcgagcctcctcaggtctcactga 1785
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QY 1786 gtgagcatgcaagcactgtagaagaagcccgaggaagaatgccaactgtgtgcaagaa 1845
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Db 1086 CCTGACTCTTCTCACTCACTGACTTCTCCCTCTCCCTACCCGCGGAGGAGCAAGTTGCG 1145
QY 1906 tgaatcaatgagccctcccaaacccggagcgttcccaagcgaagcttccctccatcctc 1965
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[illegible]

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? ORGANISM: human
? TISSUE TYPE: placenta
? IMMEDIATE SOURCE:
? LIBRARY: (F111, EMBL)
? CLONE: F1X1, F1X2, F1X3
? POSITION IN GENOME:
? FEATURE:
? PUBLICATION INFORMATION
?
US-08-377-522C-1

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Db 847 AAATGCCCGCAAGTCTTCTCTGAGTCACTCCAGCAATTAAGCCAAAGCTCTTACCA 906
1666 ggcagagcctctcgtcttgagctcaatctcttcaagcctcccaactcccaagtt 1725
907 GCGAGGACCTCTCGCTCTGAGCTCCATCTCTCTCAAGACTCTCCCAACTTCCAGGTT 966
1726 gaactcagcaagaagcctttagaaggcgagagcgcgctctcgaagtcctcaactgaa 1785
967 GAACCTACAGAGAAGCCTTTAGAAAGGCGAGAGCGCGGCTCTCGAGGTCCTCACTGAA 1026
1786 gtgaagcatgcagcaactgcaggaagcgcccgagagcaagaatgcacattgtgcaagaa 1845
1027 GTGAG-ATGCGACCACTGAGAGAACGCCCGGAGACAGAAATGTCGCAACGAA 1085
1846 cctctgactcttcttaacctgaacttcccccctccttaaccgagcgagagcaagttgc 1905
1086 CCTGACTCTTCTCTCACTGAGTCTTCCCTCTCCCTACCCGCGGCGCAAGTTGC 1145
1906 tgaatcaatgagacccctcccaaccgagcgcttcccaagcgagcttctccatctc 1965
1146 TGAATCAATGAGACCCCTCCCAACCCGCGGCTTCCAGAGAGGCTTCCCTCCATCTC 1205
1966 ctgacacacgggagcttctgtgagctcgtcttgatctgcgcagagtgacacagagt 2025
1206 CTGACCAACCGGCGCTTCTGAGCTGCTCTGATCTCGGCAAGAGTGACACACAGGT 1265
2026 gtccaagaagcgtctctggagagtgaggaagcggtttacagtgtaactgtgagtcgtc 2085
1266 GTTCAAGAGAGCTTCTTGAGAGTGAGGAAAGCGGTTTACAGTACGCTTGCTGCAAGCTC 1325
2086 agggagcgagcactgacagcaaacacacccctgagcgacccctgtgctgcagcgagact 2145
1326 AGGGGCGGCGACTGCGACGGAACACACCCCTGAGGCCAGCCCTGGGTGCCAGCGGAGCT 1385
2146 gectctctccgcgaggttggtgagcccgctcagtaegaggttgaggagagcttcttaact 2205
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2206 tggagagatgtctcaaaaacacatgtggacatctggaacctctacacctgtgtacct 2265
1446 TCGGAGGATGTCTCAAAACCAATCTGTGGCATCTGAGACCTCTCTCTGTGTGAGCCCT 1505
2266 ctctcgtcccggtgagaggttaacccgtcttaagtcgagggagataagcaagtggcgag 2325
1506 CTCTGCGCCGCGGTGAGGCTTACCCGCTTAACTGTCGCGGAGTAGCAAGTGGGCGGG 1565
2326 cgcggagacgctgagaggtgagcgagcgagcgagcgagcgagcgagcgagcgagcg 2369
1566 GCGGCGGAGC---GCGGATTCGCGCGGCGACGCGCACCGCGGCG 1606

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RESULT 9
US-08-377-522D-1

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; Sequence 1, Application US/08377522D
; GENERAL INFORMATION:
; APPLICANT: Mountz et al.
; TITLE OF INVENTION: Human Fas Gene Promoter Region
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: TX
; ZIP: 77071
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch floppy
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,522D

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; FILING DATE: January 20, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5919
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1608 bp
; TYPE: nucleic acid
; STRANDEDNESS: double-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: genomic DNA
; HYPOTHEICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: human
; TISSUE TYPE: Placental
; IMMEDIATE SOURCE:
; LIBRARY: (FIX1; EMBL-Sp6/T7
; CLONE: FIX1, FIX2, FIX3; EMBL1, EMBL2, EMBL3
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; US-08-377-522D-1

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Query Match 47.8%; Score 1536.8; DB 7; Length 1608;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1582; Conservative 0; Mismatches 17; Indels 5; Gaps 3;

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QY 767 agagatgcccataccatccctccctacccactctcttctgtctatagatctca 826
Db 7 ACAGAGATGCGCTTATACATCCCTCTTATCCCACTTTTGTGTGATGATGCTCA 66
QY 827 gagtgtgtgacaaagctgagcagccagaggtctctcactatgacactaagctactga 886
Db 67 GAGTGTGTGCAAGAGCTGTGACGCCCGAGGCTTCTCAATGCGCAACAGTCTACGA 126
QY 887 aaggttgaaagagaaagccttcaacacttaagaactgtgtgtaagtcaatgagag 946
Db 127 AAGGTGGAACAGAGACAGGCTTATCAACACTTACAGACTGTGTGATGATGACAG 186
QY 947 atgcaaaacagagtgatgaaagccctcagagaggttaacctactagatttgaaggc 1006
Db 187 ATGCAAAACAGAGGCTATGGAAGCCCTCAGAGGCTTAACCTAAGATTGAGAGGC 246
QY 1007 cc-aacaggtccagaaagaatgtcaactgagaggaagcctgaagaatgaacagtgagc 1065
Db 247 CCAACAGGCTCCAGAGAAATGTCAACTGAGAGGAAAGCTGAAGAGTGAACAGTGGGC 306
QY 1066 taagcaaaaggttattatgttattatgaatgtgtaacttaattggaaaggaagagag 1125
Db 307 TAAGCAAAAGGTTATTAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAA 366
QY 1126 ttgagagtgagtgagagcttgtagacatgcacaaaggaataactgaaccttaagt 1185
Db 367 TTGCAAGATGAGTGAGGAGGCTTGTGTGACGATGCCAAAGGAATTAACCTTTAGTG 426
QY 1186 tgtccagcttggaactgacatccaaatccaggttcaagtaatgagtcatatccaaacata 1245
Db 427 TGTCAAGTGTGAAGTCAATCCAAATTCAGGTTCAATATGATGATTCATTCACAAATCA 486
QY 1246 cctctgtaaatctcagctaaactactaagagctatcactacgttccaaagcaatagt 1305

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QY 1366 ggcgaagaataatgagtaacgaagaagaaatattgtgaattttaataatagctg 1425
Db 607 GGCAGAGAAATATGAGTAACGAAGACGAAGAACTAATGTGAATGTTTATATAGCTG 666
QY 1426 ggcatacgaatttgagtaattgtttagctttgttcccttbaagaataaactag 1485
Db 667 GGGTATGCGATTGGCTTAGTGTGTTGTTTCTTCTTGAATATATAAATAAG 726
QY 1486 gggccctcccttccagagccttaagcgcaacatcgtacttttataatgtaactg 1545
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Db 787 TCCATTCCAGGAAGTCTGTGAGCCCTCTCATGTTGACCAACAAGATGAGACGCCAGTC 846
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Db 907 GCGAGAGACTCTGCGCTGAGCTCCATCTCTCTCAAGACCTCCCAACTTCCAGGTT 966
QY 1726 gaactacaagcagaagcctttagaagaagcgagagcgagcttcgagttcctcctgaa 1785
Db 967 GAACATACAGCAAGCCTTTAGAAAGGCGAGAGGCGGCTCTGAGAGTCTCTCACTGAA 1026
QY 1786 gtgacatgccaagcagctcaggaagcgcccgagacagaaatgccattgtgcaagaa 1845
Db 1027 GTGAG-ATGCCAGCCACTGACAGAACGCCCGGACAGAGAAATCCCTTGTGCAAGAA 1085
QY 1846 cccctaccccttccctcaccctgaacttcccccctaccgagcgagccaagttgc 1905
Db 1086 CCTTACTCTCTTCTACCTTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1145
QY 1906 tgaatcaatgagccctccccaaccccgagcggttccccaagaggttccctccatctc 1965
Db 1146 TGAATCAATGAGAGCCCTCCCAACCCGGGCGTTCCCAAGAGGCTTCTTCCATCTC 1205
QY 1966 ctgacacccggggttctctgtagctcgtctcgtatctcgcgcaagagtlacacaggt 2025
Db 1206 CTGACACACGGGGCTTTCTGTAGCTCGTCTGATCTGCGCAAGAGTACACACAGGT 1265
QY 2026 gtccaagaacgcttctgggagtgagggagagcggtttagatgacttgctgtagcctc 2085
Db 1266 GTTCAAAACAGCTTCTGTGGGAGTGAAGGAGGTTTACGAGTGTGGCTGTGAGACCTC 1325
QY 2086 aggggagcgacgtgacaggaacacacccctgagcgagccctgagcgccagcgagct 2145
Db 1326 AGGGGCGGGCACTGGCAGAGAACACACCTGAGGCCAGCCCTGCTGCCAGCGAGGCT 1385
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QY 2206 tcggaagatgtctacaacaacatctgtggaatctggaacccctctactctgtgatacct 2265
Db 1446 TCGGAGAGTTTCTCAACAAACCATGCTGTGGCATGTGAGCCCTCTACTCTGTGAGACCTC 1505
QY 2266 ctctgcccgggtggaagcttaaccgctctagtcaccgggagtagcaagtgaggcgag 2325
Db 1506 CTCTTCCCGGGGTGAGAGCTTACCCGCTTATGTCCTCCGGGATAGGCAAAAGTGGGGGG 1565
QY 2326 cgcggagacgctgagatctgagcgagcgagcgagcgagcgagc 2369
Db 1566 CGCGGAGCG---GCGGAGTTGCGGGGCGACGCGCACCGCGGCG 1606

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RESULT 10
US-60-324-185-29531
; Sequence 29531, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preetl
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324, 185
; NUMBER OF SEQ ID NOS: 2001-09-21
; SOFTWARE: PERL Program
; SEQ ID NO 29531
; LENGTH: 3814
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 415714.1
US-60-324-185-29531

Query Match 24.9% Score 799.8 DB 71; Length 3814;
Best Local Similarity 99.6% Pred. No. 8,6e-163;
Matches 812; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1445 agtgttagcttgttctctctcttgaagaataaactaagggccctccctttagag 1504
Db 1 agtgttagcttgttctctctctcttgaagaataaactaagggccctccctttagag 60
QY 1505 ccttagcgcaacatctgtacttttcaatagttaactgtccattcagaagctg 1564
Db 61 ccttagcgcaacatctgtacttttcaatagttaactgtccattcagaagctg 120
QY 1565 tgaagctcctatgttgaagcgaacatgagagcccgatcaatgagcccgagctt 1624
Db 121 tgaagctcctatgttgaagcgaacatgagagcccgatcaatgagcccgagctt 180
QY 1625 ctctgagtagctccaagcaatlagccaaggtctctgtacccaagcgagacctgctct 1684
Db 181 ctctgagtagctccaagcaatlagccaaggtctctgtacccaagcgagacctgctct 240
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Db 241 gagctcaattctcttcaagaactcccaactccaggttgaactacaagaagcctt 300
QY 1745 tagaagaagcgagagcgagctctcgaaggtctcactcctgaagtgagcatgccaagctg 1804
Db 301 tagaagaagcgagagcgagctctcgaaggtctcactcctgaagtgagcatgccaagctg 360
QY 1805 caagaagccccgggagagaagatgccaattgtgtgaacgaacccgagactcttccacc 1864
Db 361 caagaagccccgggagagaagatgccaattgtgtgaacgaacccgagactcttccacc 420
QY 1865 ctgacttctccctccctaccacggcgagccaagttgctgaaatcgaatgagccctc 1924
Db 421 ctgacttctccctccctaccacggcgagccaagttgctgaaatcgaatgagccctc 480
QY 1925 caaacccgggcttccccaagagagcttctctccatctctctgaccccgagcttctc 1984
Db 481 caaacccgggcttccccaagagagcttctctccatctctctgaccccgagcttctc 540
QY 1985 gtgagctcgtctctgactctcgcaagagtlacacacaggtgttccaagagcttctgag 2044
Db 541 gtgagctcgtctctgactctcgcaagagtlacacacaggtgttccaagagcttctgag 600
QY 2045 gagtgaaggaagcggtttagagtagcttgctgagagcctcaagggcgagctgagac- 2103

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Db 601 gagtgaaggaagcgtttacagagtgacttgcgtgagcctcagagggcggaactgagaca 660
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Db 661 ggaacacaccctgaagcagccctgctgcccagggcgagctgcctcttcccgcggt 720
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Db 721 tggtagaccgcgtcagtaagagttggggaagctcttcaacttcgaggaattgacaaca 780
Qy 2224 accatgctggatctgtgacccctcctcctggt 2258
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RESULT 11
US-09-834-291-2
; Sequence 2, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Kramer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-2
Query Match 22.2%; Score 713; DB 32; Length 720;
Best Local Similarity 100.0%; Pred. No. 3.3e-144;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2560 gaagtgagcgtggggcgagcaggaattgaagcggaagcttgggaagcttaaggtcgc 2619
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Db 61 gaagtgagcgtggggcgagcaggaattgaagcggaagcttgggaagcttaaggtcgc 120
Qy 2620 tggagggagggcccggttggagagagagcggaactccttgacaagccctgaagccaa 2679
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Db 121 tggagggagggcccggttggagagagagcggaactccttgacaagccctgaagccaa 180
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Db 181 gccaaaagtcgcgtccgcgcggtgggtgggtgggtgggtgggtgggtgggtgggtgggt 240
Qy 2740 gaagctcagccttcaaaaacatatgtctatttcttgaggtcttaagagtaggaa 2799
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Db 241 gaagctcagccttcaaaaacatatgtctatttcttgaggtcttaagagtaggaa 300
Qy 2800 taagtcagcagcagcagtggttaagcggagggctcggagaaacggcaccttctt 2859
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Db 301 taagtcagcagcagcagtggttaagcggagggctcggagaaacggcaccttctt 360
Qy 2860 ctgcaaaaagtataatggggctgaatgagcttctgaggtctgttaacgtttttat 2919
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Db 361 ctgcaaaaagtataatggggctgaatgagcttctgaggtctgttaacgtttttat 420
Qy 2920 gtccacagaaagaaactcctgctccttcgggaattcctcttaagactga 2979
|||

Db 421 gtacacagaaagaaactgcgtgtcctccctccgggaattctctcttaagactga 480
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Db 481 agtcgctcctgaagtggtttcaatttgtttttcttctgcctctcttcttctt 540
Qy 3040 ccccttctgaagtggtttcaatttgtttttcttctgcctctcttcttctt 3099
|||
Db 541 ccccttctgaagtggtttcaatttgtttttcttctgcctctcttcttctt 600
Qy 3100 taactgtcccccagcagaaacccggccctatatttgccaagaacttgagcact 3159
|||
Db 601 taactgtcccccagcagaaacccggccctatatttgccaagaacttgagcact 660
Qy 3160 gtttgaagatccctcgtcagtaattgcagcttgcagatggttaatacaag 3212
|||
Db 661 gtttgaagatccctcgtcagtaattgcagatggttaatacaag 713
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RESULT 12
US-09-404-284-674/c
; Sequence 674, Application US/09404284
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 20411-780
; CURRENT APPLICATION NUMBER: US/09/404,284
; CURRENT FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 4670
; SOFTWARE: Hy-Patent.pl Version 3.1
; SEQ ID NO 674
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-404-284-674
Query Match 13.2%; Score 424.2; DB 18; Length 449;
Best Local Similarity 99.3%; Pred. No. 1.7e-81;
Matches 426; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1679 cgtctgagctcattctcttcttaagacctcccaactccaggttgtaactacagaga 1738
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Db 449 cgtctgagctcattctcttcttaagacctcccaactccaggttgtaactacagaga 390
Qy 1739 agccttgaagaagggcagagggcggtctcagagtgctcaactgaagtgaatgcag 1798
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Db 389 agccttgaagaagggcagagggcggtctcagagtgctcaactgaagtgaatgcag 330
Qy 1799 ccactgcaagaagcccgaggagaaatgcacattgtgcaacgaacactgaactctc 1858
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Db 329 ccactgcaagaagcccgaggagaaatgcacattgtgcaacgaacactgaactctc 270
Qy 1859 ctacacctgaacttccctccctaccgcgcgcagagcgaagtgtgtaataatgag 1918
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Db 269 ctacacctgaacttccctccctaccgcgcgcagagcgaagtgtgtaataatgag 210
Qy 1919 cccctcccaacccggggttccccaagaggtctccttccatctcctcgaacccggg 1978
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Db 209 cccctcccaacccggggttccccaagaggtctccttccatctcctcgaacccggg 150
Qy 1979 ctttctgtgctcgtctcgtatctgcgcgaagagtaacacaggggtttaagagct 2038
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Db 149 ctttctgtgctcgtctcgtatctgcgcgaagagtaacacaggggtttaagagct 90
Qy 2039 tctgggagtgaggaagcgggttttaagagtgacttggtcagagctcagggcgagcact 2098
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Qy 2099 ggcacggaa 2107
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Db 29 gccacggga 21

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RESULT 13
US-09-524-038-674/c
; Sequence 674, Application US/09524038
; GENERAL INFORMATION:
; APPLICANT: Dimanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark C.
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 780CIP
; CURRENT APPLICATION NUMBER: US/09/524,038
; CURRENT FILING DATE: 2000-03-13
; EARLIER APPLICATION NUMBER: 09/404,284
; EARLIER FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 4670
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 674
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-524-038-674
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Query Match 13.2% Score 424.2; DB 19; Length 449;
Best Local Similarity 99.3%; Pred. No. 1.7e-81;

Matches 426; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1739 agccttgaagagcgagagcgagctctgagtgctcccaactgagtgagagatgcag 1798
DB 389 AGCCTTTGAAAGGGCAGAGGCGCGCTTCGAGGCTCCACCTGAAGTGAAGCATGCCAG 330
QY 1799 ccaactgcagagacgcccgggagcaagatgccattgtgcagacgaacctgaactcttc 1858
DB 329 CCACGTGAGGAAGCGCCCGGGGACAGAGATGCCCATTTGTGCACAGAACCTGACTCTTC 270
QY 1859 ctcaactgactctccctccctccaccgagcgagagcgaagtgtcgaatcaatgagag 1918
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QY 1979 ctcttgtagctcgtctctgactcgcgcaagagtgacacacagtggttcaagacgct 2038
DB 149 CTTTTCGAGACTCGTCTCTGATCTCGGCAAGAGTGAACAGAGTGTTCAAAGACGT 90
QY 2039 tctggagagtgagagagagcggtttaagagtgactgtgctgagcctcaggggcgagact 2098
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DB 29 GGCACGGGA 21
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RESULT 14
US-60-324-185-9888/c
; Sequence 9888, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
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; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 9888
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 1383957.6
; NAME/KEY: unsure
; LOCATION: 1156, 1235, 1267, 1304, 1364
; OTHER INFORMATION: a, t, c, g, or other
US-60-324-185-9888
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Query Match 12.1% Score 387.4; DB 71; Length 1368;
Best Local Similarity 99.7%; Pred. No. 2.6e-73;

Matches 388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2349 gcggcagcgagcgagcgagcgagccttggaagcgagcgctgtcgtgagagcgltgagac 2408
DB 329 GCGGACAGGCGGACGCGGCGGACCTGGAGGCGCGCTGTGCGGAGGCGCTTGAGAC 270
QY 2409 tggctccggggggtgttagagacctccctcagggcgcggtgtcgaagagatgagagac 2468
DB 269 TGGCTCCCGGGGCGCTGTAGGACCTTCCCTCAGGCCCGGGTGTGAGACGCTGAGAC 210
QY 2469 ttgcttcttggtgcttgatgcagagtgatccgcttgagcagcgagcgagcgtccg 2528
DB 209 TTGCTTTCTTGCGGCTGTGATGCGAAGTGTGATCCCGCTGGGCGAGGGGCGACTCCG 150
QY 2529 gcgctcctgagagcagcagcgtccacgttgaggtgaggtgaggtgagcagagaaat 2588
DB 149 GCGCTCTCGGAGACCACTGCTCCACGTGAGTGGGCTGGGCGGCGGACAGAAAT 90
QY 2589 gaagcggagatctggaagcctttaggtgctgctgagagggagcccggttgaagagagag 2648
DB 89 GAGCGGAAGTGTGGAAGCTTTAGGGTCTGTGAGGGGAGACCCCGTTGAGAGAGAG 30
QY 2649 cggaaactcctggagaaagccttgaagcc 2677
DB 29 CGGAACCTCTGAGCAACCCCTGACAGCC 1
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RESULT 15
US-09-644-867-7725/c
; Sequence 7725, Application US/09644867
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Donovan, Michael J.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1173-001
; CURRENT APPLICATION NUMBER: US/09/644,867
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151,061
; NUMBER OF SEQ ID NOS: 8090
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7725
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
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GenCore version 4.5
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(without alignments)
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3193	99.4	45121	6 US-10-035-832-1262	Sequence 1262, App
2	424.2	13.2	449	7 US-10-011-154-674	Sequence 674, App
3	334.4	10.4	772	6 US-10-211-364-477	Sequence 477, App
4	334.4	10.4	772	7 US-10-143-906-21	Sequence 21, App
5	252	7.8	2551	1 PCT-US02-10824-85	Sequence 85, App
6	252	7.8	2551	1 PCT-US02-25766-9394	Sequence 9394, App
7	252	7.8	2551	6 US-10-035-832-1263	Sequence 1263, App
8	252	7.8	2551	7 US-10-007-926A-143	Sequence 143, App
9	226	7.0	2534	5 US-09-053-375B-233	Sequence 233, App
10	67.8	2.1	55966	6 US-10-035-832-1259	Sequence 1259, App
11	60.8	1.9	816	7 US-10-027-632-145670	Sequence 145670, App
12	60	1.9	2435	7 US-10-113-872-796	Sequence 796, App
13	60	1.9	2821	7 US-10-113-872-1669	Sequence 1669, App
14	59.2	1.8	542	7 US-10-027-632-91808	Sequence 91808, App
15	59.2	1.8	542	7 US-10-027-632-304597	Sequence 304597, App
16	59.2	1.8	639	7 US-10-027-632-134014	Sequence 134014, App
17	59.2	1.8	639	7 US-10-027-632-134015	Sequence 134015, App
18	59.2	1.8	639	7 US-10-027-632-134016	Sequence 134016, App
19	57.6	1.8	43599	1 PCT-US02-25766-10281	Sequence 10281, App
20	57.6	1.8	1350	7 US-10-011-154-201	Sequence 201, App
21	57	1.8	920	1 PCT-US02-25766-10795	Sequence 10795, App
22	56.2	1.7	975	5 US-09-954-531-998	Sequence 998, App
23	56.2	1.7	2892	1 PCT-US02-19457-103	Sequence 103, App
24	56.2	1.7	2892	7 US-10-175-523-103	Sequence 103, App
25	56	1.7	822	6 US-10-098-754-2303	Sequence 2303, App

26	55.8	1.7	1140	7 US-10-027-632-253750	Sequence 253750, App
27	55.8	1.7	1140	7 US-10-027-632-253751	Sequence 253751, App
28	55.2	1.7	443	7 US-10-027-632-64316	Sequence 64316, App
29	55.2	1.7	443	7 US-10-027-632-64317	Sequence 64317, App
30	55.2	1.7	443	7 US-10-027-632-296990	Sequence 296990, App
31	55.2	1.7	443	7 US-10-027-632-296991	Sequence 296991, App
32	54.8	1.7	1191139	5 US-09-811-352B-1	Sequence 1, App
33	54.8	1.7	1191139	7 US-10-140-924-1	Sequence 1, App
34	54.6	1.7	1527	7 US-10-011-154-202	Sequence 202, App
35	54.6	1.7	2501	7 US-10-027-632-103140	Sequence 103140, App
36	54.6	1.7	48763	1 PCT-US02-23268-3	Sequence 3, App
37	54.4	1.7	551	7 US-10-027-632-71673	Sequence 71673, App
38	54.4	1.7	1076	6 US-10-098-754-1296	Sequence 1296, App
39	54.4	1.7	44990	6 US-10-035-832-1229	Sequence 1229, App
40	54.4	1.7	44990	6 US-10-052-482-217	Sequence 12, App
41	54.2	1.7	113585	6 US-10-188-470-12	Sequence 111688, App
42	54	1.7	2759	7 US-10-027-632-111688	Sequence 1328, App
43	54	1.7	27827	6 US-10-035-832-1338	Sequence 329, App
44	53.8	1.7	375	1 PCT-US02-09239-339	Sequence 331, App
45	53.8	1.7	375	1 PCT-US02-09239-331	Sequence 331, App

ALIGNMENTS

RESULT 1
US-10-035-832-1262
; Sequence 1262, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035, 832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747, 377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798, 586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1262
; LENGTH: 45121
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-035-832-1262

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QY	61	ttccccaagaacacacacatcatttaagtggttcaataatagatcttcaagaattca	120
DB	8054	ttccccaagaacacacacatcatttaagtggttcaataatagatcttcaagaattca	8113
QY	121	aaggaagaagaagtttggaagaacatatataattaccacaccccttgacattacac	180
DB	8114	aaggaagaagaagtttggaagaacatatataattaccacaccccttgacattacac	8173
QY	181	taagggccctgagaagtttggaagaagtttcaaatlaaagtaaccagaattt	240
DB	8174	taagggccctgagaagtttggaagaagtttcaaatlaaagtaaccagaattt	8233
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DB	8234	ctaagattatttgacataaacaatgctccccaagaagacacatctctactct	8293
QY	301	gaacttgagataattagacgtaagtggtgagggtaggggaagggtatgatcataga	360

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OY 421 actaacacatcttgcgaatgtgtcttaagccttttgcctacatcttttctgttaag 480
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; LENGTH: 772
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (593)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (594)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (704)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-211-364-477
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Query Match          10.4%; Score 334.4; DB 6; Length 772;
Best Local Similarity 99.7%; Pred. No. 1.8e-61;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1923 ccccaaccggcggttccccagcagagctctccatccctctgacccacgggagctt 1982
D 9 cgcacaccggcggttccccagcagagctctccatccctctgacccacgggagctt 68
QY 1983 tcgtagctcgctctgactctcgacagagtgacacacagtggttcaagaagctctg 2042
D 69 tcgtagctcgctctgactctcgacagagtgacacacagtggttcaagaagctctg 128
QY 2043 gggagtgaggagcgggttaccagagtgacttgctgagagcctgaaggcgagctgca 2102
D 129 gggagtgaggagcgggttaccagagtgacttgctgagagcctgaaggcgagctgca 188
QY 2103 cggacacaccccttgagcagccctgctgctccagcgagcgtctctctcccgagg 2162
D 189 cggacacaccccttgagcagccctgctgctccagcgagcgtctctctcccgagg 248
QY 2163 ttgtgagcccgctcagtaagagtggtggagctcttccacttggaagattgtcaac 2222
D 249 ttgtgagcccgctcagtaagagtggtggagctcttccacttggaagattgtcaac 308
QY 2223 aaccatgctgggacatctggaacctctactctgt 2258
D 309 aaccatgctgggacatctggaacctctactctgt 344
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```

RESULT 4
US-10-143-906-21
; Sequence 21, Application US/10143906
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ/OCIN
; CURRENT APPLICATION NUMBER: US/10/143,906
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 21
; LENGTH: 772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (593)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (594)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
```

```

; NAME/KEY: misc_feature
; LOCATION: (704)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-143-906-21
```

```
Query Match          10.4%; Score 334.4; DB 7; Length 772;
Best Local Similarity 99.7%; Pred. No. 1.8e-61;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1923 ccccaaccggcggttccccagcagagctctccatccctctgacccacgggagctt 1982
D 9 cgcacaccggcggttccccagcagagctctccatccctctgacccacgggagctt 68
QY 1983 tcgtagctcgctctgactctcgacagagtgacacacagtggttcaagaagctctg 2042
D 69 tcgtagctcgctctgactctcgacagagtgacacacagtggttcaagaagctctg 128
QY 2043 gggagtgaggagcgggttaccagagtgacttgctgagagcctgaaggcgagctgca 2102
D 129 gggagtgaggagcgggttaccagagtgacttgctgagagcctgaaggcgagctgca 188
QY 2103 cggacacaccccttgagcagccctgctgctccagcgagcgtctctctcccgagg 2162
D 189 cggacacaccccttgagcagccctgctgctccagcgagcgtctctctcccgagg 248
QY 2163 ttgtgagcccgctcagtaagagtggtggagctcttccacttggaagattgtcaac 2222
D 249 ttgtgagcccgctcagtaagagtggtggagctcttccacttggaagattgtcaac 308
QY 2223 aaccatgctgggacatctggaacctctactctgt 2258
D 309 aaccatgctgggacatctggaacctctactctgt 344
```

```

RESULT 5
PCT-US02-10824-85
; Sequence 85, Application PC/TUS0210824
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Prostate Cancer Expression Profiles
; FILE REFERENCE: 90 206 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/10824
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/281,732
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/281,731
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patentl version 3.1
; SEQ ID NO 85
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-10824-85
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Query Match          7.8%; Score 252; DB 1; Length 2551;
Best Local Similarity 100.0%; Pred. No. 9.4e-44;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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D 1 gcaaggtgacacacaggttccaagaagctctgaggagtgaggagcgtttacga 60
QY 2067 gtaacttgctgagcctcagggcgagcactgacaggaacacacccctgaagccccc 2126
D 61 gtaacttgctgagcctcagggcgagcactgacaggaacacacccctgaagccccc 120
QY 2127 tggctgccagcagcagctcctctctcccgcgagtggttgagccgcctcagtaaggag 2186
D 121 tggctgccagcagcagctcctctctcccgcgagtggttgagccgcctcagtaaggag 180
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 10:21:41 ; Search time 8462.63 Seconds
(without alignments)
5122.783 Million cell updates/sec

Title: US-09-834-291-1
Perfect score: 3212
Sequence: 1 ttgagactcgcgaataatg.....ttgcagatgctcaatcaag 3212

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	710	22.1	793	10	BI763679 603049567
c 2	453.4	14.1	467	9	AA704610 zj19h02.s
c 3	386.6	12.0	899	9	AL540709 AL540709
c 4	386.4	12.0	506	10	BG659530 TGEStv2
c 5	357.8	11.1	599	10	BF569266 602185634
c 6	340.6	10.6	1140	10	BG121070 602352793
c 7	328.2	10.2	617	9	AV695647 AV695647
c 8	291.4	9.1	603	9	AA058563 zf55b04.s
c 9	287.4	8.9	577	9	AA056275 zf53q03.s
c 10	280.4	8.7	547	9	AA047220 zf49e11.s
c 11	279.4	8.7	442	9	AA011028 ze34d02.s
c 12	278.4	8.7	447	9	AA057418 zif5h03.s
c 13	276.4	8.6	467	9	AA020992 ze65f07.s
c 14	263	8.2	376	10	H84298 YS95609.s1
c 15	257	8.0	398	10	H86126 YS94608.s1
c 16	256.4	7.9	429	9	AW239285 xh38d02.y
c 17	254.4	7.9	297	9	AA018441 ze50a08.s

c 18	253	7.9	381	10	H86544 yf04f01.s1
c 19	215.4	6.7	359	9	AV692383 AV692383
c 20	214.4	6.7	1339	10	BG288747 602385566
c 21	214	6.7	932	9	AL542093 AL542093
c 22	210.4	6.6	300	9	AU100132 AU100132
c 23	202.4	6.3	1052	10	BM455788 BM455788
c 24	191	5.9	800	10	BI463384 BI463384
c 25	190	5.9	419	10	R83827 R83827
c 26	185.2	5.8	828	10	AV715411 AV715411
c 27	181.8	5.7	696	10	BI838027 BI838027
c 28	135	4.2	577	10	BM310113 BM310113
c 29	124.4	3.9	291	9	AA383161 AA383161
c 30	114.4	3.6	341	9	AA375635 AA375635
c 31	96	3.0	285	10	BM090262 505440 MA
c 32	80.4	2.5	1101	12	CNS00396 CNS00396
c 33	67	2.1	1101	12	CNS00396 CNS00396
c 34	66.4	2.1	993	12	AG090948 AG090948
c 35	66	2.1	1101	12	CNS01523 CNS01523
c 36	65.2	2.0	932	12	CNS00720 CNS00720
c 37	63.8	2.0	1027	12	CNS01677 CNS01677
c 38	63.6	2.0	306	9	AA668797 AA668797
c 39	63.6	2.0	549	9	AA521324 AA521324
c 40	63.6	2.0	583	9	AA521406 AA521406
c 41	63.4	2.0	699	10	BG076530 BG076530
c 42	63.2	2.0	1101	12	CNS0182P CNS0182P
c 43	63	2.0	698	12	AZ184604 AZ184604
c 44	63	2.0	1201	12	CNS0165X CNS0165X
c 45	62.8	2.0	987	12	CNS016F1 CNS016F1

ALIGNMENTS

RESULT 1
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603049567F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5189752 5',
LOCUS
DEFINITION
BI763679.1 GI:15755257
ACCESSION
BI763679
VERSION
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM11474 row: e column: 17
High quality sequence stop: 786.
Location/Qualifiers
1..793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5189752"
/clone.lib="NIH_MGC_116"
/lab.host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 52 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is

Db	241	AGTGCATGACAGATGCAAAACACAGGGTGATGMAAGCCCTCAGGAGGTAACCTAAC	300
QY	994	taagatttgaggccc-aacaggtctccagaagaaatgtcaactagaggaagccctgaag	1052
Db	301	TAGATTGAGGGGCCCAACAGGGCTCCGAGMAAAATGCACTGAGAGAGCCGGAAG	360
QY	1053	atgaacgttgggtccaaagcaagggtcttaatgtgtatratatggttaatcnaattgg	1112
Db	361	ATGAAACAGTGGGCTTAAGCAAAAGGCTTATTATGTGTTATTATGGGTTGAATCTTAAG	420
QY	1113	gaagagagagaggttcgaagtgaggttccaagctctgttgcagatg	1159
Db	421	GAAAGGAGAGGTTGCAGACTGAGTCCAAAGCTTGSTGGACATG	467

RESULT	LOCUS	DEFINITION	ACCESSION VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
3	AL540709/c										
	AL540709	899 bp mRNA				Homo sapiens					
	AL540709	LITL_FL002_PL1 Homo sapiens cDNA clone CS0DE002YN18				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
		, mRNA sequence.				Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	AL540709					1 (bases 1 to 899)					
	AL540709.1	GI:12871113				L.H.W.B., Gruber,C., Jesse,J. and Polayes,D.					
	EST.					Full-length cDNA libraries and normalization					
						unpublished (2001)					
						Contact: Genoscope					
						Genoscope - Centre National de Sequencage					
						Bp 191 91006 EVRI cedex - France					
						Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.					

FEATURES	SOURCE
Location/Qualifiers	1. .899
/organism="Homo sapiens"	/db_xref="taxon:9606"
/clone="CS0DE002YN18"	/clone_lib="ET1_FL002_PL1"
/lab_host="DH10B"	/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"
192 a	288 c 245 g 170 t
4	others

Query Match	12.0%	Score 385.6	DB 9	Length 899
Best Local Similarity	99.0%	Pred. NO. 3.1e-58		
Matches 397	Conservative	2	Mismatches 1	Indels 1

QY 2289 cccgctctagtcccgaggatagcgcaagtgggcggcgcgcggaacgcgtgcgggattcg 2348

400 CCGCTTTAGTCCCGGGGATAGGCAAAAGTGGGGCGGGC-CGGGACGGCTGCGGGATTGGC 342

[illegible][illegible]

Db 341 GCGGCACGGCCGACCGGACCGGCGTCGCGGAGGCGTGGAAAC 282

QY 2409 tggctcccggggctgttagaccttcctcaggcccggtgtctcagaacgatgtgaagac 2468

Db 281 TGGCTCCCCGGGGGCTT7TAGGACCTTCCTCAGGCCCGGGTCTCAGAACGCTGGAGAC 222

QY 2469 ttgctttctctgagccttgatgagaaagtgcctgatcccgctggcagggcgggcaagctccg 2528

Db	221	TTGGTTTTCCTGGGCGCTTGATGCGAAGTGTGATCCCGCTGGGCGAGCGGGCAGCTCCG	162
QY	2529	gqgcctcctcggagaagcaactgcgtccacgcttgaagltggcgltggggggcggaaggaatt	2588
Db	161	GGGTCTCCGGAGAGCACTGCGCTCCACGTTGAGGTGGCGTGGGGGGCGGACAGGAATT	102
QY	2589	gaagcggaaagtcctbvgaaagctttagtgctgcgtggaaggggagaccgcggttggagagaagag	2648
Db	101	GAAACGGGAAGTCTGGGAAGCTTTAGGGTCTGGCTGGAGGGGACCCCGTGTTGGAGAGAGGAG	42
QY	2649	cggaaactcctbvgacaagccctgacaagccaaagccaaaggtc	2689
Db	41	CGGAATCTCTGGACAAGCCCTGACAAGGCCAAGCCAAAGTTC	1

RESULT	4
LOCUS	BG659530/c
DEFINITION	BG659530 506 bp mRNA linear EST 11-MAY-2001 TGESTYyza24g01.y1 TGVEG118 Tachyzoite cDNA library Toxoplasma gondii cDNA clone TGESTYyza24g01.y1.5, similar to TR:063030 O63030 RAT ALPHA-SMOOTH MUSCLE ACTIN MRNA FRAGMENT ;, mRNA sequence.
ACCESSION	BG659530
VERSION	BG659530.1 GI:1380191
KEYWORDS	EST.
SOURCE	Toxoplasma gondii.
ORGANISM	Toxoplasma gondii. Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.
REFERENCE	1 (bases 1 to 506)
AUTHORS	Cifang,X., Cole,R., Fogarty,S., Sibley,L.D., Ajikwa,J.A., White,M., Tang,R.S., Pape,D., Martin,J., Wylie,T., Dante,M., Marr,M., Hillier,L., Kucaba,T., Theising,B., Bowers,J., Gibbons,M., Ritter E., Bennett,J., Franklin,C., Tsagarisvilli,R., Ronko,I., Kennedy S., Maguire,L., Waterston,R. and Wilson,R.

TITLE Toxoplasma EST project
JOURNAL Unpublished (2001)
COMMENT Contact: Clifton, S.
 Toxoplasma EST project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: toxo@watson.wustl.edu
 Contact David Sibley (toxosteporcim.wustl.edu) for further
 information relating to organism, libraries, or clone availability
 Seq primer: -40R from Gibco
 High quality sequence stop: 371.

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FEATURES
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    Location/Qualifiers
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        /strain="VEG"
        /db_xref="taxon:5811"
        /clone="TGESTzya24g01.y1"
        /clone_lib="TVEG118 Tachyzoite cDNA library"
        /dev_stage="Tachyzoite"
        /lab_host="DH10B"
        /note="Vector: pBluescript SK; Site 1: EcoRI; Site 2: Xho
I. This library was constructed by Keliang Tang, Robert
M. Slaughter, and Shoukat Washington. University of

```

COLE, and L. David Stiles) are WARNING: This library may contain size-selected and directionally cloned into the Uni-ZAP X lambda vector (Stratagene). The primary library was mass excised as phagemids and rescued in SOCR cells. The plasmid library was recovered from the SOCR cells and transformed in mass into DH10B (GeneHog, Research Genetic, Inc.) for sequencing. WARNING: This library may contain a small percentage contaminants from human fibroblast

BASE COUNT	cells."	
86 a	191 c	140 g
ORIGIN		89 t

Query Match	12.0%	Score 386.4	DB 10	Length 506
Best Local Similarity	99.7%	Pred. No. 3.4e-58		
Matches 387	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY 2289	ccgccttaagtc	ccgggga	taagcaaa	gttgggcg
DB 388	ccccctttatg	ccccggg	atagcaaa	gttgggcg
QY 2349	gcggcagc	gcggcagc	gcggcagc	gcggcagc
DB 328	gcggcagc	gcggcagc	gcggcagc	gcggcagc
QY 2409	tggctcccg	ggggtct	taagac	cttcctcc
DB 268	tggctcccg	ggggtct	taagac	cttcctcc
QY 2469	ttgccttct	ttggggt	atgagc	ttgagc
DB 208	ttgccttct	ttggggt	atgagc	ttgagc
QY 2529	ggcctcctg	ggagacc	atgagc	ttgagc
DB 148	ggcctcctg	ggagacc	atgagc	ttgagc
QY 2589	gaagcgaag	ctctgga	agcttga	gtctgga
DB 88	gaagcgaag	ctctgga	agcttga	gtctgga
QY 2649	cgggaactc	ctggaca	agccttga	agc
DB 28	cgggaactc	ctggaca	agccttga	agc
RESULT 5	BF569266	599 bp	mRNA	linear
LOCUS	602185634F1	NIH_MGC_45	Homo sapiens	CDNA clone IMAGE:4309953 5'
DEFINITION	mRNA sequence.			
ACCESSION	BF569266			
VERSION	BF569266.1	GI:11642749		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	NIH-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@phs-remail.nih.gov Tissue Procurement: Lineman CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L10C1184 row: C column: 10 High quality sequence stop: 595. Location/Qualifiers 1. 599 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4309953" /clone_1ib="NIH_MGC_45" /tissue_type="renal carcinoma (ascites)" /lab_host="DH10B (phage-resistant)" /note="Organ: Kidney; Vector: pOT7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California,			

BASE COUNT	ORIGIN	118 a	210 c	172 g	99 t
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Best Local Similarity		99.4%;	Pred. No. 3.7e-53;		
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DB	361	ccccctttagtc	ccccgggattgagcaaa	gtgggscggcgacgctcggttgccg	302
OY	2349	gcggcagcgagcg	cgacggcgacacctgtgag	cgggcggtctgtcggaagagcgttgagac	2408
DB	301	gcggcagcgagcg	cgacggcgacacctgtgag	cgggcggtctgtcggaagagcgttgagac	242
OY	2409	tgagtcgccggggg	ggtctgttagagaccttc	ccctcaggccgggtgctcagaagatgagagac	2468
DB	241	tgagtcgccggggg	ggtctgttagagaccttc	ccctcaggccgggtgctcagaagatgagagac	182
OY	2469	ttgctttctctgg	ggccttgatgcgaagt	ctgtatcccgctggggagagcgggcgagtcgcg	2528
DB	181	ttgctttctctgg	ggccttgatgcgaagt	ctgtatcccgctggggagagcgggcgagtcgcg	122
OY	2529	gcgcctctcgga	gacacctgcgctccacg	tttaggtgtggtgtggggcgagcagaat	2588
DB	121	gcgcctctctcgga	gacacctgcgctccacg	tttaggtgtggtgtggggcgagcagaat	62
OY	2589	gaagcggagagct	gtggaaagctttaggtgt	gcgtcgggaaggagaccccggttggaagagagag	2648
DB	61	gaagcggagagct	gtggaaagctttaggtgt	gcgtcgggaaggagaccccggttggaagagagag	2
OY	2649	c	2649		
DB	1	c	1		
RESULT	6	BG121070/c	1140 bp	mRNA	linear
LOCUS	602352793F1	NIH_MGC_90	Homo sapiens	CDNA clone	IMAGE:4451039 5'
DEFINITION	602352793F1	NIH_MGC_90	Homo sapiens	CDNA clone	IMAGE:4451039 5'
ACCESSION	BG121070				
VERSION	BG121070.1	GI:12614579			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
TITLE	1 (bases 1 to 1140)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgrabbs-r@mail.nih.gov				
	Tissue Procurement: ATCC				
	CDNA Library Preparation: Life Technologies, Inc.				
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNL at:				
	http://image.llnl.gov				
	Plate: L1AM10237	row: 1	column: 24		
	High quality sequence start: 9				
	High quality sequence stop: 727.				
FEATURES	location/Qualifiers				
source	1..1140				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:4451039"				

VERSION AA047220.1 GI:1525120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoso, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W., Hawkins, M., Hollman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierly-Meg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
JOURNAL MEDLINE
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 893 Std Error: 0.00
Seq primer: -40M13 fwd. from Amerham
High quality sequence stop: 471.
Location/Qualifiers
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/db_xref="GDB:128857"
/db_xref="taxon:9606"
/clone="IMAGE:380300"
/clone_lib="Soares retina N2b4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pRT3D (Pharmacia) with a modified polylinker; Site: 1; Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 131 a 128 c 125 g 158 t 5 others
ORIGIN
Query Match 8.7%; Score 280.4; DB 9; Length 547;
Best Local Similarity 99.3%; Pred. No. 1.6e-39;
Matches 292; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 2980 agtcgctgcctgaagttcatttttttttttttttttttttttttttttt 3039
DB 61 AGTCGCTGCCTGAATGTTTGTGTTTCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 3040 ccccttctgctgctgctccatgctgctgctgctgctgctgctgctgctgctg 3099
DB 121 CCCCTTCTTGAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 3100 tactcgttccacacgacagacccgctctattatgtgccaagaacttagagacct 3159

DB 181 TACTGCTCCACACGACAGAAACCGCGCCCTATTATTGGCCAGAACTTGACGACCT 240
QY 3160 gtttgaagaagtcctcgtcgaagaatgccagcttgc-agatgctcaatcaag 3212
DB 241 GTTTGAAAAGTCCCTCCGCTGCAATGCGACCTTGCAAGATGGCAATCAAG 294
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DEFINITION IMAGE:360867 3', mRNA sequence.
ACCESSION AA011028
VERSION AA011028.1 GI:1472055
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hollman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
JOURNAL MEDLINE
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
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High quality sequence stop: 372.
Location/Qualifiers
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/clone_lib="Soares retina N2b4HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pRT3D (Pharmacia) with a modified polylinker; Site: 1; Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 92 a 107 c 103 g 138 t 2 others
ORIGIN
Query Match 8.7%; Score 279.4; DB 9; Length 442;
Best Local Similarity 99.0%; Pred. No. 2.4e-39;
Matches 291; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 2920 gtacacagaagaagaaactgcctgtctccctccgggaattctcttaagact-gt 2978
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25 32 25.6 13/1 / 05-10-158

Sequence 2736, AF

APPLICANT: SU

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Query Match      100.0%; Score 125; DB 6; Length 45121;
Best Local Similarity 100.0%; Pred. NO. 3e-22;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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      |||||||
Db 10494 gatccgcctggagcagagcgagcgagctccgcgcctcctcgagagaccactgcgtccacggt 10553
OY      61 gaggtgggscgtctgggggggcgagacaggaattgaaacggaagctctgggaagctttaaggctcgc 120
      |||||||
Db 10554 gaggtgggscgtctgggggggcgagacaggaattgaaacggaagctctgggaagctttaaggctcgc 10613
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Db 10614 tggag 10618

RESULT      2
PCT-US02-25766-3153
; Sequence 3153, Application PC/TUS025766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E
; APPLICANT: FAULK, Ronald
; APPLICANT: SUN, Hongwei

```

```
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/311,837
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3153
; LENGTH: 4657
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. L36818
PCT-US02-25766-3153
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Query Match          29.3%; Score 36.6; DB 1; Length 4657;
Best Local Similarity 58.9%; Pred. No. 2.9;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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QY 3 tccgcgtggcagcgcgagctccgcgcctcctcgcagaccactgcgtccacgttga 62
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Db 4262 ttcaaccggcctgaaccacagcgagagctccgtaagaccctcccccgcgtgg 4321
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QY 63 ggtggcgctggggcgagcagcaatggaagcggaagctgtggaagc 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4322 ggtggggcggggtgtcgtccggaatggaagataagcccgagacc 4368
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```
RESULT 3
US-10-018-407A-1
; Sequence 1, Application US/10018407A
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-2 EXPRESSION
; FILE REFERENCE: RSP-0039
; CURRENT APPLICATION NUMBER: US/10/018,407A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/339,964
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 4743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(3988)
US-10-018-407A-1
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Query Match          29.3%; Score 36.6; DB 7; Length 4743;
Best Local Similarity 58.9%; Pred. No. 2.9;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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QY 3 tccgcgtggcagcgcgagctccgcgcctcctcgcagaccactgcgtccacgttga 62
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Db 4348 ttcaaccggcctgaaccacagcgagagctccgtaagaccctcccccgcgtgg 4407
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QY 63 ggtggcgctggggcgagcagaaatgaacggaagctgtggaagc 109
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Db 4408 ggtggggcggggtgtcgtccggaatgaagaaatagcccgagacc 4454
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RESULT 4
PCT-US02-23766-55/c
; Sequence 55, Application PC/TUS0223766
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; GENERAL INFORMATION:
; APPLICANT: Le, Wei-dong
; APPLICANT: Vassiliadis, Demetrios K
; TITLE OF INVENTION: Mutant Nurrl Gene in Parkinson's Disease
; FILE REFERENCE: P02512W01
; CURRENT APPLICATION NUMBER: PCT/US02/23766
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,294
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 10883
; TYPE: DNA
; ORGANISM: Human
PCT-US02-23766-55
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Query Match          27.0%; Score 33.8; DB 1; Length 10883;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 56; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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QY 16 gcggggcagctccgcgcctcctcgcagaccactgcgtccacgttgagtggtggg 75
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5688 GCAGGGCAGCTTCGGCGGAGCCCGGAGAGCTGGGCAGTCCCGGAGAGCTGGGCTGGGC 5629
```

```
QY 76 gcggagcaggaatggaagcggaagctgtggaag 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5628 TACTGGCACCAAGCGAGGGCAGACACTCCGAGG 5596
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```
RESULT 5
US-10-205-951-55/c
; Sequence 55, Application US/10205951
; GENERAL INFORMATION:
; APPLICANT: Le, Wei-dong
; APPLICANT: Vassiliadis, Demetrios K
; TITLE OF INVENTION: Mutant Nurrl Gene in Parkinson's Disease
; FILE REFERENCE: P02512W01
; CURRENT APPLICATION NUMBER: US/10/205,951
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,294
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 10883
; TYPE: DNA
; ORGANISM: Human
US-10-205-951-55
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```
Query Match          27.0%; Score 33.8; DB 6; Length 10883;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 56; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5688 GCAGGGCAGCTTCGGCGGAGCCCGGAGAGCTGGGCAGTCCCGGAGAGCTGGGCTGGGC 5629
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```
QY 76 gcggagcaggaatggaagcggaagctgtggaag 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5628 TACTGGCACCAAGCGAGGGCAGACACTCCGAGG 5596
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RESULT 6
US-10-137-113-12/c
; Sequence 12, Application US/10137113
; GENERAL INFORMATION:
; APPLICANT: Kepur, Vivek
; APPLICANT: Bannantine, John P.
; TITLE OF INVENTION: Mycobacterial Diagnostics
; FILE REFERENCE: 09531-112001
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; CURRENT APPLICATION NUMBER: US/10/137,113
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/362,396
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Mycobacterium paratuberculosis
; US-10-137-113-12

Query Match 26.6%; Score 33.2; DB 6; Length 1110;
Best Local Similarity 64.1%; Pred. No. 21;
Matches 50; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 gatccgcgtgagcagcgagcgtcctcctcgtcagcagcgtcgcctcagcgtt 60
|| || || || || || || || || || || || || || || || || || || || ||
Db 645 GAGACCGGGGGTGTGGCGGCAAGACACGCGCGGCTTGATTCACAGGTGCTGACGAT 586
|| || || || || || || || || || || || || || || || || || || || ||
Qy 61 gagctgggcgtgaggagc 78
|| || || || || || || || || || || || || || || || || || || || ||
Db 585 GCGGTGGCCACGACGAGAC 568

RESULT 7

US-09-918-995-29556/C
; Sequence 29556, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29556
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-29556

Query Match 26.2%; Score 32.8; DB 5; Length 465;
Best Local Similarity 59.8%; Pred. No. 27;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 15 ggcggggcagcgtcgcgtcctcctcgtcagcagcgtcagcgttgaagtgagcgtgag 74
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Db 453 GGGGGGGAAGCTGAGAGGCTGGGCGACGACGCGCCCGCTTGAGTTGGGGGCTGCGGCTCGG 394
|| || || || || || || || || || || || || || || || || || || || ||
Qy 75 ggcggcagcaggaattgaagcgcgaagtcgtgga 106
|| || || || || || || || || || || || || || || || || || || || ||
Db 393 GGACGGGGCTGGGTGAAGGCGACGCGCTGGGA 362

RESULT 8

US-10-211-625-47/C
; Sequence 47, Application US/10211625
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM034CIN
; CURRENT APPLICATION NUMBER: US/10/211,625
; CURRENT FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: 09/758,468
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 2114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1432)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc.feature
; LOCATION: (2012)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc.feature
; LOCATION: (2066)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (2109)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc.feature
; LOCATION: (2113)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-211-625-47

Query Match 26.2%; Score 32.8; DB 6; Length 2114;
Best Local Similarity 59.8%; Pred. No. 26;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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Qy 75 ggcggcagcaggaattgaagcgcgaagtcgtgga 106
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Db 1628 GGACGGGGCTGGGTGAAGGCGACGCGCTGGGA 1597

RESULT 9

US-09-646-569-178
; Sequence 178, Application US/09646569
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERNI
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE
; FILE REFERENCE: ALBRE 8
; CURRENT APPLICATION NUMBER: US/09/646,569
; CURRENT FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00909
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: DE 198 13 835.0
; PRIOR FILING DATE: 1998-03-20
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 178
; LENGTH: 3265
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-646-569-178

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3395, 3437, and 3440
OTHER INFORMATION: N-G,A,C or T
US-10-018-311A-1

Query Match 26.2%; Score 32.8; DB 7; Length 3768;
Best Local Similarity 55.2%; Pred. No. 25;
Matches 64; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 9 tgggagagcgagcgagcgtccgagcgtctctcgagagcactgcgtccagctgaggtgag 68
DB 703 tgggagagcgagcgagcgtccgagcgtctctcgagagcactgcgtccagctgaggtgag 762
QY 69 cgtgggggagcgagcaggaattgaagcggaagctctggaagccttaaggctgcgtgga 124
DB 763 ggcagagctcgccgcgcgcgtgaaagggaaccgcagagcgagcgagcgagctgga 818

RESULT 14
US-09-919-002-3827
Sequence 3827, Application US/09919002
GENERAL INFORMATION:
APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
PRIOR FILING DATE: FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3827
LENGTH: 7318
TYPE: DNA
ORGANISM: Homo sapiens
US-09-919-002-3827

Query Match 26.2%; Score 32.8; DB 5; Length 7318;
Best Local Similarity 59.8%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 15 ggcggggagcagctccgagcgtctctcgagagcactgcgtccagctgaggtgagcgtgag 74
DB 1105 ggtggggagaggtgagggcgtgagcagagcccgagcgtgagcgtgaggtgagcgtgag 1164
QY 75 gggcgagcaggaattgaagcgagcgtgagga 106
DB 1165 ggaaggggagcgtgaggtgaggaagcagcgtgagga 1196

RESULT 15
PCT-US02-23766-1/C
Sequence 1, Application PC/US0223766
GENERAL INFORMATION:
APPLICANT: Le, Wei-dong
APPLICANT: Vassilatis, Demetrios K
TITLE OF INVENTION: Mutant Nurrl Gene in Parkinson's Disease
FILE REFERENCE: P02512MO1
CURRENT APPLICATION NUMBER: PCT/US02/23766
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/308,294
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.1

SEQ ID NO 1
LENGTH: 9824
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(9824)
OTHER INFORMATION: n = unknown
PCT-US02-23766-1

Query Match 26.2%; Score 32.8; DB 1; Length 9824;
Best Local Similarity 59.1%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 16 ggcgggagcagcgtccgagcgtctctcgagagcactgcgtccagctgaggtgagcgtgag 75
DB 4563 GCAGGGACGCTTCGGCGGAGCCCGGAGAGCTGGCGAGTCCCGGAGAGCTGGCGTGGGC 4504
QY 76 ggcgagcaggaattgaagcggaagctggaag 108
DB 4503 TACTGGCACCAAGGCAGAGGGCACACANTCCGAG 4471

Search completed: September 8, 2002, 01:10:21
Job time: 37099 sec

2

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 22:32:03 ; Search time 13836.9 Seconds
(without alignments)
195.445 Million cell updates/sec

Title: US-09-834-291-2_COPY_1_125
Perfect score: 125
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2	125	100.0	318	25	US-09-652-127-2780	Sequence 2780, Ap
3	125	100.0	324	17	US-09-396-087-4122	Sequence 4122, Ap
4	125	100.0	720	32	US-09-834-291-2	Sequence 2, Appl
5	125	100.0	1368	71	US-60-324-185-9888	Sequence 9888, Ap
6	125	100.0	1732	25	US-09-644-867-7725	Sequence 7725, Ap
7	125	100.0	1732	25	US-09-652-911-10283	Sequence 10283, A
8	125	100.0	3212	32	US-09-834-291-1	Sequence 1, Appl
9	125	100.0	45121	36	US-09-997-722-10	Sequence 10, Appl
10	123.4	98.7	419	18	US-09-489-036-818	Sequence 818, App
11	123.4	98.7	419	35	US-09-943-143-818	Sequence 818, App
12	123.4	98.7	575	17	US-09-471-275-3315	Sequence 3315, Ap
13	121.8	97.4	404	17	US-09-362-510-3927	Sequence 3927, Ap
14	121.8	97.4	404	17	US-09-362-510A-3927	Sequence 3927, Ap
15	121.8	97.4	404	34	US-09-904-013-3927	Sequence 3927, Ap
16	112.4	89.9	1555	56	US-60-172-373-10224	Sequence 10224, A
17	112	89.6	495	25	US-09-652-911-4924	Sequence 94, Appl
18	109.4	87.5	2165	25	US-09-665-615B-94	Sequence 94, Appl
19	109.4	87.5	2165	31	US-09-802-669-94	Sequence 847, App
20	101.8	81.4	362	19	US-09-522-303-847	Sequence 9889, App
21	101.8	81.4	362	23	US-09-617-081-898	Sequence 1341, Ap
22	95	76.0	443	25	US-09-522-303-1341	Sequence 8181, Ap
23	89.2	71.4	2760	25	US-09-644-865-8181	Sequence 8055, Ap
24	89.2	71.4	2760	25	US-09-652-124-8055	Sequence 7930, Ap
25	89.2	71.4	2760	25	US-09-652-816-7672	Sequence 7672, Ap
26	89.2	71.4	2760	25	US-09-652-911-8889	Sequence 8889, Ap
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29	85	68.0	355	18	US-09-431-517-12091	Sequence 12154, A
30	85	68.0	371	18	US-09-489-036-24990	Sequence 24990, A
31	85	68.0	371	35	US-09-943-143-24990	Sequence 24990, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 32 63 50.4 408 16 US-09-289-768-1798 Sequence 1798, Ap
C 33 63 50.4 408 35 US-09-939-397-1798 Sequence 1798, Ap
C 34 38.4 30.7 51 56 US-60-172-373-10226 Sequence 10226, A
35 38.2 30.6 786 25 US-09-652-128-9418 Sequence 9418, Ap
36 37.8 30.2 438 17 US-09-306-350A-34407 Sequence 34407, A
37 37.8 30.2 438 34 US-09-909-629-34407 Sequence 34407, A
38 37.2 29.8 396 17 US-09-359-067-35264 Sequence 35264, A
39 36.6 29.3 360 17 US-09-359-067-30849 Sequence 30849, A
40 36.6 29.3 423 17 US-09-362-510-36229 Sequence 36229, A
41 36.6 29.3 423 17 US-09-362-510A-36229 Sequence 36229, A
42 36.6 29.3 423 34 US-09-904-013-36229 Sequence 36229, A
43 36.6 29.3 475 17 US-09-359-067-35265 Sequence 35265, A
44 36.6 29.3 2963 30 US-09-760-475-1176 Sequence 1176, Ap
45 36.6 29.3 4657 11 US-08-731-233A-1 Sequence 1, Appli
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ALIGNMENTS

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RESULT 1
US-09-834-291-32
; Sequence 32, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834, 291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-32
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Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 gatcccgctgggagcgagcgagctccgagctcctcgagagaccactgagctccagctt 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 gatcccgctgggagcgagcgagctccgagctcctcgagagaccactgagctccagctt 60
QY 61 gaggtggcgctggggggcgagacgaattgaagcgagagctctgggaagctttaaggtcgc 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 gaggtggcgctggggggcgagacgaattgaagcgagagctctgggaagctttaaggtcgc 120
QY 121 tggag 125
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Db 121 tggag 125
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RESULT 2
US-09-652-127-2780/c
; Sequence 2780, Application US/09652127
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USPS
; FILE REFERENCE: 1600.1183-001
; CURRENT APPLICATION NUMBER: US/09/652, 127
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,134
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 10475
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2780
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-127-2780
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Query Match 100.0%; Score 125; DB 25; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 gatcccgctgggagcgagcgagctccgagctcctcgagagaccactgagctccagctt 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 GATCCCGCTGGGAGGCGGAGGAGCTCCGGCGCTCTCGAGACACACGCTCCACGCTT 100
QY 61 gaggtggcgctggggggcgagacgaattgaagcgagagctctgggaagctttaaggtcgc 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 99 GAGGTGGCGCTGGGGGCGGAGACGAATTGAAGCGAGAGTGTGGAGCTTTAGGGTTCG 40
QY 121 tggag 125
| | | | |
Db 39 TGGAG 35
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```
RESULT 3
US-09-396-087-4122/c
; Sequence 4122, Application US/09396087
; GENERAL INFORMATION:
; APPLICANT: Geating, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: MLN98-39pm
; CURRENT APPLICATION NUMBER: US/09/396, 087
; CURRENT FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 60/100,260
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 60/107,226
; EARLIER FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 60/131,810
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5220
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4122
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-396-087-4122
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```
Query Match 100.0%; Score 125; DB 17; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gatcccgctgggagcgagcgagctccgagctcctcgagagaccactgagctccagctt 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 149 GATCCCGCTGGGAGGCGGAGGAGCTCCGGCGCTCTCGAGACACACTGCGCTCACGTT 90
QY 61 gaggtggcgctggggggcgagacgaattgaagcgagagctctgggaagctttaaggtcgc 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 GAGGTGGCGCTGGGGGCGGAGACGAATTGAAGCGGAGAGCTTTAGGGTTCG 30
QY 121 tggag 125
| | | | |
Db 29 TGGAG 25
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RESULT 4
US-09-834-291-2
; Sequence 2, Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
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QY 1 gatcccgctggcgaagcgagcgtccgctcctcgagaccactgctccacgtt 60
Db 178 gatcccgctggcgaagcgagcgtccgctcctcgagaccactgctccacgtt 119

QY 61 gaggtggcgctggggggcgagcagaattgaagcggaaatctctggaagcttaaggtcgc 120
Db 118 gaggtggcgctggggggcgagcagaattgaagcggaaatctctggaagcttaaggtcgc 59

QY 121 tggag 125
Db 58 tggag 54

RESULT 8
US-09-834-291-1
; Sequence 1 Application US/09834291
; GENERAL INFORMATION:
; APPLICANT: Krammer, Peter
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3212
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1

Query Match 100.0%; Score 125; DB 32; Length 3212;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcccgctggcgaagcgagcgtccgctcctcgagaccactgctccacgtt 60
Db 2500 gatcccgctggcgaagcgagcgtccgctcctcgagaccactgctccacgtt 2559

QY 61 gaggtggcgctggggggcgagcagaattgaagcggaaatctctggaagcttaaggtcgc 120
Db 2560 gaggtggcgctggggggcgagcagaattgaagcggaaatctctggaagcttaaggtcgc 2619

QY 121 tggag 125
Db 2620 tggag 2624

RESULT 9
US-09-997-722-10
; Sequence 10 Application US/09997722
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RME/DCP
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 45121
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-10

Query Match 100.0%; Score 125; DB 36; Length 45121;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatcccgctggcgaagcgagcgtccgctcctcgagaccactgctccacgtt 60
Db 10494 gatcccgctggcgaagcgagcgtccgctcctcgagaccactgctccacgtt 10553

QY 61 gaggtggcgctggggggcgagcagaattgaagcggaaatctctggaagcttaaggtcgc 120
Db 10554 gaggtggcgctggggggcgagcagaattgaagcggaaatctctggaagcttaaggtcgc 10613

QY 121 tggag 125
Db 10614 tggag 10618

RESULT 10
US-09-489-036-818
; Sequence 818 Application US/09489036
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 783
; CURRENT APPLICATION NUMBER: US/09/489,036
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 35324
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 818
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-036-818

Query Match 98.7%; Score 123.4; DB 18; Length 419;
Best Local Similarity 99.2%; Pred. No. 7.1e-21;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatcccgctggcgaagcgagcgtccgctcctcgagaccactgctccacgtt 60
Db 107 gatcccgctggcgaagcgagcgtccgctcctcgagaccactgctccacgtt 166

QY 61 gaggtggcgctggggggcgagcagaattgaagcggaaatctctggaagcttaaggtcgc 120
Db 167 gaggtggcgctggggggcgagcagaattgaagcggaaatctctggaagcttaaggtcgc 226

QY 121 tggag 125
Db 227 tggag 231

RESULT 11
US-09-943-143-818
; Sequence 818 Application US/0943143
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 783
; CURRENT APPLICATION NUMBER: US/09/943,143
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/489,036
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 35324
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 818
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LENGTH: 419
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-143-818

Query Match 98.7%; Score 123.4; DB 35; Length 419;
Best Local Similarity 99.2%; Pred. No. 7, 1e-21;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatccgcgtggcagggcagggcagctccgctcctcgcgagacgactgcgtccacgtt 60
|||
Db 107 gaccgcgcgtggcagggcagggcagctccgctcctcgcgagacgactgcgtccacgtt 166
|||
QY 61 gaggtggcgcgtggcggcgagacgaggaattgaagcggaagctctgggaagctttagggctcgc 120
|||
Db 167 gaggtggcgcgtggcggcgagacgaggaattgaagcggaagctctgggaagctttagggctcgc 226
|||
QY 121 tggag 125
|||
Db 227 tggag 231

RESULT 12
US-09-471-275-3315/c

Sequence 3315, Application US/09471275
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Contigs Obtained
FILE REFERENCE: 782
CURRENT APPLICATION NUMBER: US/09/471,275
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: US 09/234,611
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: US 09/240,371
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US 09/277,227
EARLIER FILING DATE: 1999-03-25
EARLIER APPLICATION NUMBER: US 09/271,490
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: US 09/293,972
EARLIER FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: US 09/274,861
EARLIER FILING DATE: 1999-03-23
EARLIER APPLICATION NUMBER: US 60/125,453
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/126,605
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: US 09/306,350
EARLIER FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/399,720
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10451
SOFTWARE: pt_ct_genes Version 1.0
SEQ ID NO 3315
LENGTH: 575
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (465)...(578)
OTHER INFORMATION: similar to g1178067 in the genepept database release 114,
OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-471-275-3315

Query Match 98.7%; Score 123.4; DB 18; Length 575;
Best Local Similarity 99.2%; Pred. No. 7, 1e-21;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gatccgcgtggcagggcagggcagctccgctcctcgcgagacgactgcgtccacgtt 60
|||
Db 313 GACCCGCTGGGCGACAGCGGGGCGAGCTCCGGCCCTCTCGGAGACCACTCGCGTCCACGTT 254
|||
QY 61 gaggtggcgcgtggcggcgagacgaggaattgaagcggaagctctgggaagctttagggctcgc 120
|||
Db 253 GAGGTGGCGCTGGGCGGCGGACAGCAATTTGAAGCGGAAGCTCTGGGAAGCTTTAGGGTCCG 194
|||
QY 121 tggag 125
|||
Db 193 TGGAG 189

RESULT 13
US-09-362-510-3927/c

Sequence 3927, Application US/09362510
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362,510
EARLIER FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 09/221,820
EARLIER FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 62165
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3927
LENGTH: 404
TYPE: DNA
ORGANISM: Homo sapiens
US-09-362-510-3927

Query Match 97.4%; Score 121.8; DB 17; Length 404;
Best Local Similarity 98.4%; Pred. No. 1, 8e-20;
Matches 123; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gatccgcgtggcagggcagggcagctccgctcctcgcgagacgactgcgtccacgtt 60
|||
Db 174 GACCCGCTGGGCGACAGCGGGGCGAGCTCCGGCCCTCTCGGAGACCACTCGCGTCCACGTT 115
|||
QY 61 gaggtggcgcgtggcggcgagacgaggaattgaagcggaagctctgggaagctttagggctcgc 120
|||
Db 114 GAGGTGGCGCTGGGCGGCGGACAGCAATTTGAAGCGGAAGCTCTGGGAAGCTTTAGGGTCCG 55
|||
QY 121 tggag 125
|||
Db 54 TGGAG 50

RESULT 14
US-09-362-510A-3927/c

Sequence 3927, Application US/09362510A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-759CON1
CURRENT APPLICATION NUMBER: US/09/362,510A
EARLIER FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 09/221,820
NUMBER OF SEQ ID NOS: 62165
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3927
LENGTH: 404
TYPE: DNA
ORGANISM: Homo sapiens

EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1999-02-16

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: EARLIER APPLICATION NUMBER: 60/120,254
:
: EARLIER FILING DATE: 1999-02-16

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; FEATURE:
; OTHER INFORMATION: PLASMID POS3410H57
US-09-017-706-4

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
Best Local Similarity 54.4%; Pred. No. 10;
Matches 56; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Oy 1 gatccgcgtggcagcgccgagcgtccgcgtcctcctcgagacacactgctccagctt 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1451 gatcgagcgccagcgacgagatgctgtccgcacccgcttatgcgcgcgatccacgctc 1510

Oy 61 gaggtgagcgctggggggcgacaggaattgaagcggaagctcg 103
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Db 1511 ggtgcgcgcacgcgcagcacgcagcagtgtagcagtgctcag 1553

RESULT 6
US-09-017-706-5
; Sequence 5, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTAASE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; OTHER INFORMATION: PLASMID POS3410U57
US-09-017-706-5

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
Best Local Similarity 54.4%; Pred. No. 10;
Matches 56; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Oy 1 gatccgcgtggcagcgccgagcgtccgcgtcctcctcgagacacactgctccagctt 60
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Db 1451 gatcgagcgccagcgacgagatgctgtccgcacccgcttatgcgcgcgatccacgctc 1510

Oy 61 gaggtgagcgctggggggcgacaggaattgaagcggaagctcg 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1511 ggtgcgcgcacgcgcagcacgcagcagtgtagcagtgctcag 1553

RESULT 7
US-09-017-706-6
; Sequence 6, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTAASE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; OTHER INFORMATION: PLASMID: POS3410H139
US-09-017-706-7

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
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; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; FEATURE:
; OTHER INFORMATION: PLASMID: POS3410F139
US-09-017-706-6

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
Best Local Similarity 54.4%; Pred. No. 10;
Matches 56; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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Db 1451 gatcgagcgccagcgacgagatgctgtccgcacccgcttatgcgcgcgatccacgctc 1510

Oy 61 gaggtgagcgctggggggcgacaggaattgaagcggaagctcg 103
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Db 1511 ggtgcgcgcacgcgcagcacgcagcagtgtagcagtgctcag 1553

RESULT 8
US-09-017-706-7
; Sequence 7, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTAASE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; OTHER INFORMATION: PLASMID: POS3410H139
US-09-017-706-7

Query Match          22.2%; Score 27.8; DB 3; Length 1981;
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TELEPHONE: 312-715-1000

	TELEFAX:	312-715-1234	
	TELEX:	810-221-8317	
	INFORMATION FOR SEQ ID NO:	12:	
	SEQUENCE CHARACTERISTICS:		
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	TYPE:	NUCLEIC ACID	
	STRANDEDNESS:	singl e	
	TOPOLOGY:	linear	
	MOLECULE TYPE:	DNA (genomic)	
	FEATURE:		
	NAME/KEY:	exon	
	LOCATION:	1..803	
	IDEN TIFICATION METHOD:	/evidence= experimental	
	OTHER INFORMATION:	/evidence= EXPERIMENTAL	
	OTHER INFORMATION:	/standard_name= "Alternate Exon 3: D4.7"	
	OTHER INFORMATION:	/note= "This sequence represents the third exon of allele D4.7 of the human D4 dopamine receptor gene"	
	FEATURE:		
	NAME/KEY:	misc_feature	
	LOCATION:	257..262	
	IDEN TIFICATION METHOD:	/function= "Psi site"	
	OTHER INFORMATION:	/evidence= EXPERIMENTAL	
	OTHER INFORMATION:	/standard_name= "Psi site"	
	OTHER INFORMATION:	/label= PsiI	
	OTHER INFORMATION:	/note= "This sequence is a PsiI site whereby digestion of human genomic DNA produces a RFLP"	
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	NAME/KEY:	repeat_region	
	LOCATION:	346..682	
	IDEN TIFICATION METHOD:	/rpt_type= "tandem"	
	OTHER INFORMATION:	/evidence= EXPERIMENTAL	
	OTHER INFORMATION:	/rpt_unit= 346 .. 394	
	OTHER INFORMATION:	/note= "This sequence is a repeat found in 7 known alleles of the human D4 dopamine receptor gene OTHER INFORMATION: encoding a 16 amino acid sequence repeated 7 times	
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	LOCATION:	2..803	
	US-07-928-611-12		
	Query Match	22.1%;	Score 27.6; DB 1; Length 803;
	Best Local Similarity	60.8%;	Pred. No. 9.7;
	Matches	62; Conservative	0; Mismatches 39; Indels 1; Gaps 1
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Dd	561 ccccgccgaaggccgccccggggccgcacacctgcgggcccgcaggcggtttcgaggag	502	
QY	65 -tgggcgtcgggggcgcaacaagaattgaagcgaagatctggy	105	
bD	501 CCGGCGCCGGGGGCCACAGTCGGGC CGCAGGGTCCGGG	460	
	- -		
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	US-08-487-811A-12/c		
	: Sequence 12, Application US/08487811A		
	: Patent No. 5883226		
	: GENERAL INFORMATION:		
	: APPLICANT: Civelli, Olivier		
	: APPLICANT: Van Tol, Hubert H.M.		
	: TITLE OF INVENTION: A NO. 5883226el Human Dopamine Receptor and Uses		
	: NUMBER OF SEQUENCES: 24		
	: CORRESPONDENCE ADDRESS:		
	: STREET: McDonnell Boehnen Hulbert & Berghoff,		
	: CITY: Chicago		
	: STATE: IL		
	: COUNTRY: USA		
	: ZIP: 60606		

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,811A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5883226nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: exon
LOCATION: 1..803
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /standard_name="Alternate Exon 3: D4.7"
OTHER INFORMATION: /note="This sequence represents the third exon of
OTHER INFORMATION: allele D4.7 of the human D4 dopamine receptor
FEATURE:
NAME/KEY: misc_feature
LOCATION: 257..262
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OTHER INFORMATION: /function="Psi site"
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /standard_name="Psi site"
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OTHER INFORMATION: /note="This sequence is a Psi site whereby
OTHER INFORMATION: digestion of human genomic DNA produces a RFLP"
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OTHER INFORMATION: /note="This sequence is a repeat found in 7 known
OTHER INFORMATION: alleles of the human D4 dopamine receptor gene
OTHER INFORMATION: encoding a 16 amino acid sequence repeated 7 times
FEATURE:
NAME/KEY: CDS
LOCATION: 2..803
US-08-487-811A-12

Query Match 22.1%; Score 27.6; DB 2; Length 803;
Best Local Similarity 60.8%; Pred. No. 9.7;
Matches 62; Conservative 0; Mismatches 39; Indels 1; Gaps
OY 5 ccgctggcagcgcgagcagctccgcgcctctcggagaccactgcgtccacgttgg 64
Db 561 CCCCGGGAAGCGCGCGCGCGCGCGCGCGCGCACATCGCGGCCGCGCAGGGGTCCTGGGGAGG 502
OY 65 -tgggctgggggcgcgagcaggaattgaagcggagtctgg 105
Db 501 CCGGGCGCGGGGCGCACAGTCGGGGCGCGCACAGGGGTCGGCGG 460

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RESULT 13

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US-09-060-694-12/c
Sequence 12 Application US/09060694
Patent No. 6203998
GENERAL INFORMATION:
APPLICANT: Civeilli, Olivier
APPLICANT: Van Tol, Hubert H.M.
TITLE OF INVENTION: A No. 6203998e1 Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,694
FILING DATE: 15-APR-1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 6203998nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092-MM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 803 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: exon
LOCATION: 1..803
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /note="this sequence represents the third exon of
OTHER INFORMATION: allele D4.7 of the human D4 dopamine receptor
OTHER INFORMATION: gene"
FEATURE:
NAME/KEY: misc.feature
LOCATION: 257..262
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="Psi site"
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /standard.name="Psi site"
OTHER INFORMATION: /label="Psi
OTHER INFORMATION: /note="this sequence is a Psi site whereby
OTHER INFORMATION: digestion of human genomic DNA produces a RFLP"
FEATURE:
NAME/KEY: repeat_region
LOCATION: 346..682
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /rpt.type="tandem"
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /rpt.unit=346..394
OTHER INFORMATION: /note="this sequence is a repeat found in 7 known
OTHER INFORMATION: alleles of the human D4 dopamine receptor gene
OTHER INFORMATION: encoding a 16 amino acid sequence repeated 7 times"
NAME/KEY: CDS
LOCATION: 2..803
US-09-060-694-12

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Query Match	22.1%	Score 27.6	DB 4	Length 803
Best Local Similarity	60.8%	Pred. No. 9.7		
Matches	62	Conservative	0	Mismatches 39; Indels 1; Gaps 1.
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Db	561	CCCCGGGGAAGGCCGGGCGCGGGGGGGCGCACAGTGGGGGCCGCAAGGGGTCTGGGGGAGG	502	
Oy	65	-tgagcgtgtggtggtgcgacaggaattgaagcgcgaagctctggg	105	
Db	501	CCGGGCGGGGGGGGGCGCACAGTGGGGGCCGCGAGGGGTCGGGG	460	

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1 RESULT 14
2 PCT-US93-07370-12/c
3 : Sequence 12, Application PC/TUS930370
4 : GENERAL INFORMATION:
5 : APPLICANT:
6 : TITLE OF INVENTION: A Novel Human Dopamine Receptor and Uses
7 : NUMBER OF SEQUENCES: 22
8 : COMPUTER READABLE FORM:
9 : MEDIUM TYPE: Floppy disk
10 : COMPUTER: IBM PC compatible
11 : OPERATING SYSTEM: PC-DOS/MS-DOS
12 : SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
13 : CURRENT APPLICATION DATA:
14 : APPLICATION NUMBER: PCT/US93/07370
15 : INFORMATION FOR SEQ ID NO: 12:
16 : SEQUENCE CHARACTERISTICS:
17 : LENGTH: 803 base pairs
18 : TYPE: nucleic acid
19 : STRANDEDNESS: single
20 : TOPOLOGY: linear
21 : MOLECULE TYPE: DNA (genomic)
22 : FEATURE:
23 : NAME/KEY: exon
24 : LOCATION: 1..803
25 : IDENTIFICATION METHOD: experimental
26 : OTHER INFORMATION: /evidence=EXPERIMENTAL
27 : OTHER INFORMATION: /standard_name="Alternate Exon 3: D4.7"
28 : OTHER INFORMATION: /note="This sequence represents the third exon of
29 : OTHER INFORMATION: allele D4.7 of the human D4 dopamine receptor
30 : OTHER INFORMATION: gene"
31 : FEATURE:
32 : NAME/KEY: misc-feature
33 : LOCATION: 257..262
34 : IDENTIFICATION METHOD: experimental
35 : OTHER INFORMATION: /function="Psi site"
36 : OTHER INFORMATION: /evidence=EXPERIMENTAL
37 : OTHER INFORMATION: /standard_name="Psi site"
38 : OTHER INFORMATION: /label1="Psi
39 : OTHER INFORMATION: /note="This sequence is a psi site whereby
40 : OTHER INFORMATION: digestion of human genomic DNA produces a RFLP"
41 : FEATURE:
42 : NAME/KEY: repeat_region
43 : LOCATION: 346..682
44 : IDENTIFICATION METHOD: experimental
45 : OTHER INFORMATION: /rpt_type="tandem"
46 : OTHER INFORMATION: /evidence=EXPERIMENTAL
47 : OTHER INFORMATION: /rpt_unit=346 .. 394
48 : OTHER INFORMATION: /note="This sequence is a repeat found in 7 known
49 : OTHER INFORMATION: alleles of the human D4 dopamine receptor gene
50 : OTHER INFORMATION: encoding a 16 amino acid sequence repeated 7 times
51 : FEATURE:
52 : NAME/KEY: CDS
53 : LOCATION: 2..803
54 : PCT-US93-07370-12

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Query Match	22.1%;	Score	27.6;	DB	5;	Length	803;
Best Local Similarity	60.8%;	Pred. No.	9.7;				
Matches	62;	Conservative	0;	Mismatches	39;	Indels	1;
						Gaps	1.

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Dd 561 cccggggaaagccggccggggggggcgacacatgcggggccgcggggctcctggggagc 502a

QY 65 -tggcgctggggggcgagacgaattgaacggaatccttgg 105
Dd 501 cccggccggggggcgacacatccggggcccgacggggctccggg 460

Db 1002 CCGGGCGGGGGGCGCACAGTCGGGGCCCGCAGGGGTCGGG 961

Search completed: September 7, 2002, 18:23:12
Job time: 28886 sec

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RESULT 15
US-08-056-051-5/c
/ Sequence 5, Application US/08056051
/ Patent No. 551683
/ GENERAL INFORMATION:
/ APPLICANT: Grandy, David K
/ APPLICANT: Bunzow, James R
/ APPLICANT: Ciavelli, Olivier
/ APPLICANT: Van Tol, Hubert H.-M.
/ TITLE OF INVENTION: A NO. 551683a1 Human Dopamine Receptor and Uses
/ NO. 551683a1
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Allegretti & Witcoff, Ltd.
/ STREET: 10 South Wacker Drive, Suite 3000
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/056,051
/ FILING DATE: 19930429
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: NO. 551683nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 90,1092-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-715-1000
/ TELEFAX: 312-715-1234
/ TEXT: 910-221-5317
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1610 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: 1..103
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: 1508..1610
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 104..1507
/ US-08-056-051-5

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	Query Match	62.1%	Score 27.6;	DB 1;	Length 1610;
	Best Local Similarity	60.8%;	Pred. No. 11;		
	Matches	62;	Conservative	0;	Mismatches 39; Indels 1; Gaps 1.
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Dd	1062	ccccgggaaaagcccggcgccggcgaccaccaatgrrggggccgcacaggagggcrccrctggsgcgaag	1003		
OY	65	-tgggcgltgggggagcgagacagaattgaacgcgaagctctgg	105	.	

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 18:40:33 ; Search time 1139.19 Seconds
(without alignments)
188.392 Million cell updates/sec

Title: US-09-834-291-2_COPY_1_125
Perfect score: 125
Sequence: 1 gatccgcctggcagcgcggg.....aagcttagggcgcgtgag 125

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	266	21	AA288700 Human CD95 recepto
2	36.6	29.3	4743	21	AA291408 Human SHIP-2 nucle
3	32.8	26.2	3768	21	AA281955 Human Meg-3 CDNA.
4	32.8	26.2	3995	22	AA268201 Human osteoclast e
5	32.4	25.9	1110	22	AA229777 Human cytoskeletal
6	32.4	25.9	1110	22	AA201443 Human reproductive
7	32.2	25.8	1388	21	AA244059 Zea mays DNA fragm
8	32	25.6	511	22	AA292251 Human cDNA 5'-end
9	32	25.6	511	22	AA293511 Human cDNA clone r

10	32	25.6	1371	22	AA298822 Human cytoskeletal
11	32	25.6	1371	22	AA205199 Human reproductive
12	32	25.6	1544	22	AA294547 Human full-length
13	32	25.6	1553	19	AA294361 Human secreted pro
14	31.6	25.3	1485	16	AA287721 Human auxiliary cy
15	31.6	25.3	1485	16	AA287722 Human auxiliary cy
16	31.6	25.3	1485	17	AA283887 Human cytochrome p
17	31.6	25.3	1485	17	AA283888 Human cytochrome p
18	31.6	25.3	1485	17	AA274409 Human derived cyto
19	31.6	25.3	1485	17	AA276954 Human derived cyto
20	31.6	25.3	1485	22	AA276957 Human liver cell s
21	31.6	25.3	1758	22	AA254472 Genetic construct
22	31.6	25.3	8537	22	AA276962 DNA encoding novel
23	31.4	25.1	647	23	AA290936 2.301 kb SW-MHC-pr
24	31	24.8	2301	18	AA288426 Human secreted pro
25	30.6	24.5	1180	20	AA221112 Streptomyces venez
26	30.6	24.5	1662	18	AA262457 HSV-2 strain SB5 C
27	30.6	24.5	2056	19	AA262142 Drosophila melanog
28	30.6	24.5	2262	22	AA219753 Human cDNA 5'-end
29	29.8	23.8	776	22	AA291993 Human cDNA clone r
30	29.8	23.8	776	22	AA293732 Human CDNA clone r
31	29.8	23.8	842	22	AA294082 Primer specific fo
32	29.8	23.8	2244	23	AA276156 DNA encoding novel
33	29.8	23.8	2244	23	AA276184 DNA encoding novel
34	29.8	23.8	2410	22	AA294348 Human full-length
35	29.8	23.8	3593	22	AA293879 Human cDNA encodin
36	29.8	23.8	4569	23	AA291752 Drosophila melanog
37	29.6	23.7	1551	22	AA205562 Human secreted pro
38	29.6	23.7	1769	21	AA244492 Zea mays DNA fragm
39	29.6	23.7	3665	22	AA205513 Human secreted pro
40	29.6	23.7	1554	22	AA273537 Human immune/haema
41	29.6	23.7	15115	22	AA215261 Human nervous syst
42	29.4	23.5	1371	23	AA274912 DNA encoding novel
43	29.4	23.5	1371	23	AA274912 DNA encoding novel
44	29.4	23.5	1371	23	AA285776 DNA encoding novel
45	29.4	23.5	1372	23	AA289212 DNA encoding novel

ALIGNMENTS

RESULT 1	AA288700	standard: DNA; 266 BP.
ID	AA288700	
XX	AA288700;	
AC		
XX		
DT	11-MAY-2000	(first entry)
XX		
DE	Human CD95 receptor intron 1 fragment.	
XX		
KW	p53; CD95 receptor; human; screening; apoptosis-modulation;	
KW	Cancer chemotherapy; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	protein_bind	160..179
FT		/*tag= a
FT		/bound_moiety= p53
XX		
PN	DE1984779-C1.	
XX		
PD	03-FEB-2000.	
XX		
PF	16-OCT-1998;	98DE-1047779.
XX		
PR	16-OCT-1998;	98DE-1047779.
XX		
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	
XX		
PI	Krammer P, Mueller-Schilling M, Oren M;	
XX		

DR WPI: 2000-162245/15.
XX Novel receptor DNA useful for identifying apoptosis-modulating
PT substances potentially useful for cancer chemotherapy -
XX
PS Claim 2; Fig 4; 12pp; German.
XX This invention describes a novel p53-binding region of a human CD95
CC receptor DNA molecule. The p53-binding region, or a vector containing
CC it, can be used to screen for apoptosis-modulating substances
CC potentially useful for cancer chemotherapy. This sequence represents a
CC fragment of the human CD95 receptor intron 1 which contains a p53 binding
CC region described in the method of the invention.
XX
SQ Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;

Query Match 100.0%; Score 125; DB 21; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatccgcgtggcagcggcgagctccgcgtctctcggagacacactgcgtccagctt 60
DB 1 gatccgcgtggcagcggcgagctccgcgtctctcggagacacactgcgtccagctt 60
QY 61 gaagctggcgctggggggcgagcaagattgaagcggaagctctgggaagctttaggtcgc 120
DB 61 gaagctggcgctggggggcgagcaagattgaagcggaagctctgggaagctttaggtcgc 120
QY 121 tggag 125
DB 121 tggag 125

RESULT 2
AAZ91408
ID AAZ91408 standard; cDNA; 4743 BP.
XX
AC AAZ91408;
XX
DT 22-MAY-2000 (first entry)
XX
DE Human Ship-2 nucleotide sequence SEQ ID NO:1.
XX
KW Human; Ship-2; antisense oligonucleotide; phosphorothioate; detection;
KW Inhibition; SH2-containing phosphatidylinositol phosphatase-2; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 212..3988
FT /tag= a
FT /product= "Ship-2"
XX
PN US6025198-A.
XX
PD 15-FEB-2000.
XX
PF 25-JUN-1999; 99US-0339964.
XX
PR 25-JUN-1999; 99US-0339964.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM;
XX
DR WPI: 2000-181819/16.
DR P-PSDB; AAT80120.
XX
PT Antisense oligonucleotides, useful for inhibiting human Ship-2
PT expression and for detecting nucleic acids encoding Ship-2 -
XX
PS Example 13; Column 41-52; 34pp; English.

XX The present invention describes phosphorothioate antisense
CC oligonucleotides that specifically hybridize with, and inhibit the
CC expression of, nucleic acids encoding human Ship-2 (also called
CC SH2-containing phosphatidylinositol phosphatase-2). Also described
CC is a method of inhibiting the expression of Ship-2 in human cells
CC or tissues in vitro comprising contacting the cells with the
CC phosphorothioate antisense oligonucleotides. The phosphorothioate
CC antisense oligonucleotides can be used to treat animals (especially
CC humans) suspected of having or being prone to a disease or condition
CC associated with Ship-2 expression. The present sequence encodes
CC human Ship-2.
XX
SQ Sequence 4743 BP; 939 A; 1466 C; 1448 G; 890 T; 0 other;

Query Match 29.3%; Score 36.6; DB 21; Length 4743;
Best Local Similarity 58.9%; Pred. No. 0.31;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 tccgcgtggcagcggcgagctccgcgtctctcggagacacactgcgtccagcttga 62
DB 4348 ttccaccgggcttgaccacagcgagagagctccgctagaagctccaccgccgtgg 4407
QY 63 ggtggcgctggggggcgagcaagattgaagcggaagctctgggaagc 109
DB 4408 ggtggcgctggggggcgagcaagattgaagcggaagctctgggaagc 4454

RESULT 3
AAC81955
ID AAC81955 standard; cDNA; 3768 BP.
XX
AC AAC81955;
XX
DT 01-MAR-2001 (first entry)
XX
DE Human Meg-3 cDNA.
XX
KW Meg-3; human; mesangial kidney cell; treatment; diagnosis; renal;
KW antidiabetic; vaccine; gene therapy; pathogenesis; kidney disease;
KW glomerulonephritis; diabetes; proliferation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 53..2254
FT /tag= a
FT /product= "Meg-3"
XX
PN WO200066729-A1.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-JP02831.
XX
PR 30-APR-1999; 99JP-0123561.
XX
PA (KURO/) KUROKAWA K.
PA (MIYA/) MIYATA T.
XX
PI Miyata T;
XX
DR WPI: 2000-687536/67.
DR P-PSDB; AAB11456.
XX
PT Meg-3 protein expressed in mesangial kidney cells for diagnosis and
PT treatment of kidney disease -
XX
PS Claim 4; Page 44-53; 65pp; Japanese.
XX
CC This invention describes a novel protein highly expressed in mesangial
CC kidney cells which has renal and antidiabetic activity and which can be

PR 22-AUG-2000; 2000US-0227182
PR 23-AUG-2000; 2000US-0227009

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PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244826.
PR 01-NOV-2000; 2000US-0244827.
PR 08-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244675.
PR 08-NOV-2000; 2000US-0244676.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.

PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251989.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2000US-0259678.

(HUMAN-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI: 2001-476182/51.
P-PSDB; AAU18515.

Novel isolated human cytoskeletal element-related polypeptide useful
for diagnosis/treatment of neoplastic disorders, disorders associated
with neural transmission, chromosomal abnormalities, autoimmune
disorders -
PS Claim 1; SEQ ID No 18; 505pp; English.

XX Sequences AAS29770-AAS29813 represent cDNA molecules, which encode the
CC cytoskeletal element-related polypeptides of the invention. Cytoskeletal
CC polypeptides and their associated polynucleotides are useful in the
CC diagnosis, treatment and prevention of various types of disorders in e.g.
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by determining the presence or
CC absence of a mutation in a cytoskeletal polynucleotide. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma. The polypeptides can also be used
CC to aid wound healing, to prevent skin aging due to sunburn, to maintain
CC organs before transplantation, to regenerate tissues and in chemotaxis.
CC The polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities.
CC Note: The sequence data for this patent did not form part of the printed

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Query Match 25.9%; Score 32.4; DB 22; Length 1110;
Best Local Similarity 54.1%; Pred. No. 4;
Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 3 tccgcgtggcagcggcgccctcgcgcctcgcgcacacacgcgcgcacacgtt 62
Db 716 TCCGCTGCGCCAGGACGACCTTCAGGAGCTCCCTGATGTCCTCCGCGCCACCTGGA 657
QY 63 gctggcgctggggcgacagcaagattgaagcggaagtcgtggaagcttaggtgcgtc 122

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Db 656 GCTTGTCAGTCGCGGAGGAGTAACCTCAAGATGGGAGAGTCAGGTGACCG 597
Qy 123 ga 124
Db 596 CA 595

RESULT 6
AAL01443/c
ID AAL01443 standard; cDNA: 1110 BP.

XX AAL01443;
AC
XX 21-NOV-2001 (first entry)
DT
XX Human reproductive system related antigen cDNA SEQ ID NO: 1444.
DE Human reproductive system related antigen; reproductive system disorder;
KW Human; gene therapy: ss.
XX
OS Homo sapiens.
XX
PN W0200155320-A2.
PD
XX 02-AUG-2001.
PE
XX 17-JAN-2001; 2001WO-US01339.
PR
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205151.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 14-JUL-2000; 2000US-0218290.
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PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225758.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
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PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.
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PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239397.
PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
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PR 20-OCT-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246476.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
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PR 17-NOV-2000; 2000US-0249212.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.

PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251472.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-465570/50.
DR P-PSDB; AAM93473.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen -
PT is used in preventing, treating or ameliorating a medical condition -
XX
PS Claim 1; SEQ ID NO 1444; 1297/bp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a coding sequence of the
CC invention.
XX
SQ Sequence 1110 BP; 221 A; 322 C; 349 G; 210 T; 8 other;
XX
Query Match 25.9%; Score 32.4; DB 22; Length 1110;
Best Local Similarity 54.18; Pred. No. 4;
Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
XX
QY 3 tccgcgtggcagggcgagcgtcctcctcgtgagagaccactggcctcaagtga 62
DB 716 tgcgcgtggcagggcgagcgtcctcctcgtgagagaccactggcctcaagtga 657
QY 63 ggtggcggtggcgagcgtcctcctcgtgagagaccactggcctcaagtga 122
DB 656 gcttgggactgcctggcgagcgtcctcctcgtgagagaccactggcctcaagtga 597
QY 123 ga 124
DB 596 CA 595
XX
RESULT 7
AAC44059/c
ID AAC44059 standard; DNA; 1388 BP.
XX
AC AAC44059;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 41471.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.

XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127452.
PR 06-APR-1999; 99US-0128254.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 11-MAY-1999; 99US-0134256.
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PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
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PR 01-JUN-1999; 99US-0137222.
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PR	16-SEP-1999;	99US-0154039.
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PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
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PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158233.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
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PR	13-OCT-1999;	99US-0159295.
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PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
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PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161365.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

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Best Local Similarity	57.4%;	Pred. No. 4.7;		
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Db	154	ggcgctgcgctcgtgcgcggccctcttcgctgcgcgcgggtggaggcgagcgaga	95	
Oy	79	ggacaggaattgaagcgggaagctcgtgggaagctttaagtcg	119	
Db	94	cgagacgggattgacggcgcggaggggatccgaattctgc	54	
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ID	AAK92251	standard; cDNA; 511 bp.		
XX				
AC	AAK92251;			
XX				
DT	06-NOV-2001	(first entry)		
XX				
DE	Human cDNA 5'-end sequence, SEQ ID NO: 711.			
XX				
KW	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.			
XX				
OS	Homo sapiens.			
XX				
PN	EP130094-A2.			
XX				
PD	05-SEP-2001.			
XX				

PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
XX
PR 11-JAN-2000; 2000JP-0118774.
XX
PR 02-MAY-2000; 2000JP-0183765.
XX
XX (HELI-) HELIX RES INST.
PA
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2001-524255/58.
XX
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
PS Claim 2; SEQ ID NO 711; 1380bp + sequence listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5' - and 3'-ends of the cDNA
XX molecules have been determined. Primers for synthesizing the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesised by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence is the nucleotide
XX sequence of the 5'-end of a cDNA provided in the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 511 BP; 77 A; 173 C; 180 G; 78 T; 3 other;
XX
Query Match 25.6%; Score 32; DB 22; Length 511;
Best Local Similarity 55.4%; Pred. No. 4.7;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
XX
QY 5 ccgcctggcagcgcgagcagctccgcgcctccctcgagaccacatgcgcctccacgttagg 64
DB 309 CCGCGGGGCGACAGCCGGGACACAGGTGACACACCGCGGTGTCCTCCACGCGCG 250
XX
QY 65 tgggcgtggggggcgagcaggaattgaagcggaagctctgggaagcttagg 116
DB 249 AGGTGGGCGACCGCGGGCGACGCGGTGGCTGGCAGACCGCGGGCGCAGAGGG 198
XX
RESULT 9
AAK93511/C
ID AAK93511 standard; cDNA; 511 BP.
XX
XX AAK93511;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human cDNA clone representative sequence, SEQ ID NO: 1971.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
XX Homo sapiens.
XX
XX EP1130094-A2.
XX
XX
XX 05-SEP-2001.
XX
XX PD 07-JUL-2000; 2000EP-0114089.
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XX PF 08-JUL-1999; 99JP-0194486.
XX
XX PR 11-JAN-2000; 2000JP-0118774.
XX
XX PR 02-MAY-2000; 2000JP-0183765.
XX
XX PA (HELI-) HELIX RES INST.
XX
XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2001-524255/58.
XX
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
PS Example 11; SEQ ID NO 1971; 1380bp + sequence listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5' - and 3'-ends of the cDNA
XX molecules have been determined. Primers for synthesizing the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesised by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence was used as the
XX representative sequence from a human clone which was used in
XX homology searches to identify the clone.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 511 BP; 77 A; 173 C; 180 G; 78 T; 3 other;
XX
Query Match 25.6%; Score 32; DB 22; Length 511;
Best Local Similarity 55.4%; Pred. No. 4.7;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
XX
QY 5 ccgcctggcagcgcgagcagctccgcgcctccctcgagaccacatgcgcctccacgttagg 64
DB 309 CCGCGGGGCGACAGCCGGGACACAGGTGACACACCGCGGTGTCCTCCACGCGCG 250
XX
QY 65 tgggcgtggggggcgagcaggaattgaagcggaagctctgggaagcttagg 116
DB 249 AGGTGGGCGACCGCGGGCGACGCGGTGGCTGGCAGACCGCGGGCGCAGAGGG 198
XX
RESULT 10
AAS29822
ID AAS29822 standard; DNA; 1371 BP.
XX
XX AAS29822;
XX
XX 21-NOV-2001 (first entry)
XX
XX Human cytoskeletal element-related polypeptide encoding genomic DNA #9.
XX
XX DE
XX XX Cytoskeletal element-related protein; human; mouse; rabbit; goat; horse;
XX cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
XX cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
XX ophtalmological; vulnecary; gene therapy; autoimmune disease; neoplasm;
XX hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
XX cerebrovascular disorder; nervous system disorder; bacterial infection;
XX fungal infection; viral infection; ocular disorder; endocrine disorder;
XX gastrointestinal disorder; renal disorder; respiratory disorder;
XX wound healing; skin aging; organ transplantation; food preservative;
XX tissue regeneration; anti-infertility; food additive;
XX
XX Homo sapiens.
XX
XX XX
XX XX WO200155168-A1.
XX
XX PN 02-AUG-2001.
XX
XX PD 17-JAN-2001; 2001WO-US01331.
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XX PF 31-JAN-2000; 2000US-0179065.
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XX PR 04-FEB-2000; 2000US-0180628.
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XX PR 24-FEB-2000; 2000US-0184664.
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PR 02-MAR-2000; 2000US-0186350.
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PR 17-MAR-2000; 2000US-0190076.
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PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
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PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
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PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
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PR 06-SEP-2000; 2000US-0230438.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237038.
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PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
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PR 05-DEC-2000; 2000US-0256719.
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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476182/51.

Novel isolated human cytoskeletal element-related polypeptide useful
for diagnosis/treatment of neoplastic disorders, disorders associated
with neutral transmissiion, chromosomal abnormalities, autoimmune
disorders -
Claim 1; SEQ ID No 107; 505bp; English.

RESULT 13
AAV43618/c
ID AAV43618 standard; DNA; 1553 BP.
XX
AC AAV43618;
XX
DT 24-SEP-1998 (first entry)
XX
Human secreted protein 18 encoding DNA.
XX
Secreted protein; human; cell proliferation; cytokine activity;
KW tissue growth; cellular differentiation; regeneration; activin;
KW inhibin; chemotactic; haemostatic; thrombolytic; tumour inhibition;
XX anti-inflammatory activity; biomarker; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 65..1495
FT /tag=a
FT /product="human secreted protein"
XX
PN WO9825959-A2.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22787.
XX
PR 11-DEC-1996; 96US-0032757.
XX
PA (CHIR) CHIRON CORP.
XX
PI Escobedo J, Garcia P, Hu Q, Kothakota S, Williams LT;
DR WPI; 1998-348453/30.
XX
P-PSDB; AAW63698.
XX
Secreted human polypeptides - having cytokine, cell proliferation or
PT differentiation, activin or inhibin, tumour inhibition or
PT anti-inflammatory activities
XX
Claim 6; Pages 45-46; 78pp; English.
XX
This DNA encodes a human secreted protein. The specification provides
CC secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic
CC acid sequences shown in AAV43601 to AAV43619. The invention provides a
CC method of identifying a secreted polypeptide which is modified by rough
CC microsomes. The secreted proteins can be used in assays to determine
CC biological activities, such as cytokine, cell proliferation, or cellular
CC differentiation activities, tissue growth or regeneration, activin or
CC inhibin activity, chemotactic or chemokinetic activity, haemostatic or
CC thrombolytic activity, receptor/ligand activity, tumour inhibition, or
CC anti-inflammatory activity. The proteins can also be used as
CC biomarkers, to identify tissues or cell types which express the proteins,
CC or a stage- or disease-specific alteration in protein expression. They
CC can be used in protein interaction assays, to identify ligands or binding
CC proteins. Compounds which affect the biological activities of the
CC secreted proteins or their ability to interact with specific ligands can
CC be identified using the proteins in screening assays. The proteins and
CC antibodies that bind specifically to the protein can also be used to
CC design diagnostic tests and therapeutic compositions for diseases which
CC may be associated with altered expression of these proteins. Fusion
CC proteins comprising, e.g. signal sequences or transmembrane domains of
CC the proteins can be used to target other protein domains to cellular
CC membrane or they can be secreted extracellularly.
XX
Sequence 1553 BP; 348 A; 384 C; 467 G; 354 T; 0 other;

Query Match 25.6%; Score 32; DB 19; Length 1553;
Best Local Similarity 55.4%; Pred. No. 5.4;

Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
OY 5 ccgctggcagcgggcgagctccgcgcctctcgagaccactgcgtccagttgagg 64
DB 287 cccggggcgagcagccgcaacagcgacagctgcaaacacgcggctggtccacgcgc 228
OY 65 tgggcgtggggcgagcaggaattgaagcggagcttgggaagctttagg 116
DB 227 aggtggcgacggcgggcgacgcctggcgctggcagaccggcgagaggg 176

RESULT 14
AA087721
ID AA087721 standard; cDNA; 1485 BP.
XX
AC AA087721;
XX
DT 14-NOV-1995 (first entry)
XX
Human auxillary cytochrome P450 species 2A6 coding region.
XX
DE Human auxillary cytochrome P450 species 2A6 coding region.
XX
KW Human cytochrome P450; amplification; PCR; primer; expression vector;
KW yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
KW carcinogen; mutagen; liver metabolism; ds.
XX
OS Homo sapiens.
XX
FN EP644267-A.
XX
PD 22-MAR-1995.
XX
PF 20-JUL-1994; 94EP-0111298.
XX
PR 21-JUL-1993; 93JP-0180246.
PR 20-JUL-1993; 93JP-0201120.
PR 30-JUL-1993; 93JP-0208279.
XX
PA (HAYASHI) HAYASHI K.
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Hayashi K, Kaneko H, Komai K, Nakatsuka I, Sakaki T;
PI Yabusaki Y;
XX
DR WPI; 1995-116991/16.
XX
P-PSDB; AAR72367.
XX
Evaluation of safety of a chemical cpd. - using recombinant yeast
PT expressing human cytochrome P450 and a yeast NADPH-P450 reductase
XX
Examples; Page 49-51; 124pp; English.
XX
The nucleotide sequence of the cDNA coding region for the human
CC auxillary cytochrome P450 species 2A6. The gene encodes a protein of 494
CC amino acids. The cDNA was amplified by PCR using the primers AA087751-4.
CC The product was cloned into the yeast expression vectors PAH5N or PAHRR
CC to produce the vectors P2A6 for the expression of the cytochrome P450
CC alone or P2A6R for co-expression with the yeast NADPH-P450 reductase.
CC The vectors are used in a method for evaluating the safety of a chemical
CC compound by reacting the chemical compound with recombinantly produced
CC human cytochrome P450 molecular species 1A2 (AA087714), 2C9 (AA087715),
CC 2E1 (AA087716), or 3A4 (AA087717) or their auxillary species and
CC variants (AA087718-32), and yeast NADPH-P450 reductase, either as a fused
CC protein or in cell extracts, and analysing the resulting metabolite to
CC assess the safety of the chemical compound. The method is useful for
CC determining whether the chemical compound, or its metabolite, will be
CC converted into a carcinogenic or mutagenic form through metabolism in the
CC liver.
XX
Sequence 1485 BP; 327 A; 430 C; 413 G; 315 T; 0 other;

Query Match 25.3%; Score 31.6; DB 16; Length 1485;
Best Local Similarity 58.5%; Pred. No. 7;

us-09-834-291-2_copy_1_125.rng

RESULT	15
AAQ87722	
ID	AAQ87722 standard; cDNA; 1485 BP.
XX	

	key	location/Qualifiers
FT	variation	1427
FT		/tag= a
FT		/note= "G to A change in variant 1 changes amino acid from Arg to Lys"
XX		

PD	22-MAR-1995.
XX	
PF	20-JUL-1994; 94EP-0111298.
XX	

PR 21-JUL-1993; 93JP-0180246;
PR 20-JUL-1993; 93JP-0201120;
PR 30-JUL-1993; 93JP-0208279.

PA (HAYA/) HAYASHI K.
PA (SUMO) SUMITOMO CHEM CO LTD.
PA

PI Hayashi K, Kaneko H, Komai K, Nakatsuka I, Sakaki T,
PI Yabusaki Y;

DR WPI; 1995-116991/16.
DR P-PSDB; AAQ87722.
XX

Examples; Page 53-55; 124pp; English.

The nucleotide sequence of the cDNA coding region for the human auxiliary cytochrome P450 species 2A6 variant 1. The gene contains a change at base 1427 from A to C as compared to the wild type sequence (AA087721). This changes the amino acid residue from Arg to Lys. The cDNA was amplified by PCR using the primers AA087751-1. The product was cloned into the yeast expression vectors pAAH5N or pAAHR to produce the vectors p2A6 variant 1 for the expression of the cytochrome P450 alone or p2A6R variant 1 for co-expression with the yeast NADPH-P450 reductase. The vectors are used in the method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced human cytochrome P450 molecular species 1A2 (AA087714), 2C9 (AA087715), 2E1 (AA087716), or 3A4 (AA087717) or their auxiliary species and variants (AA087718-32), and yeast NADPH-P450 reductase, either as a fused protein or in cell extracts, and analysing the resulting metabolite to assess the safety of the chemical compound. The method is useful for determining whether the chemical compound, or its metabolite, will be

Query Match	25.3%	Score 31.6;	DB 16;	Length 1485;
Best Local Similarity	58.5%;	Pred. No. 7;		
Matches 55; Conservative	0;	Mismatches 39;	Indels 0;	Gaps 0

QY 6 cgcctgggcaagcgggagagctccggcgcctctcggaaacactgcgtccagctttaggt 65
 Db 360 cggggaagcgcgcgaagcagctccggcgtctctccatccgcacccctggggagcttcgggt 419
 QY 66 gggcgttggggcgacacaggaattgaagcgggaag 99
 Db 420 gggcgaagcggagctcgaaggagcgcaccccggaag 453

Search completed: September 7, 2002, 18:40:35
Job time: 29929 sec

